



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 03:58 PM UTC

PDB ID : 6XU8 / pdb_00006xu8
EMDB ID : EMD-10624
Title : Drosophila melanogaster Ovary 80S ribosome
Authors : Hopes, T.; Agapiou, M.; Norris, K.; McCarthy, C.G.P.; OConnell, M.J.;
Fontana, J.; Aspden, J.L.
Deposited on : 2020-01-17
Resolution : 3.00 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

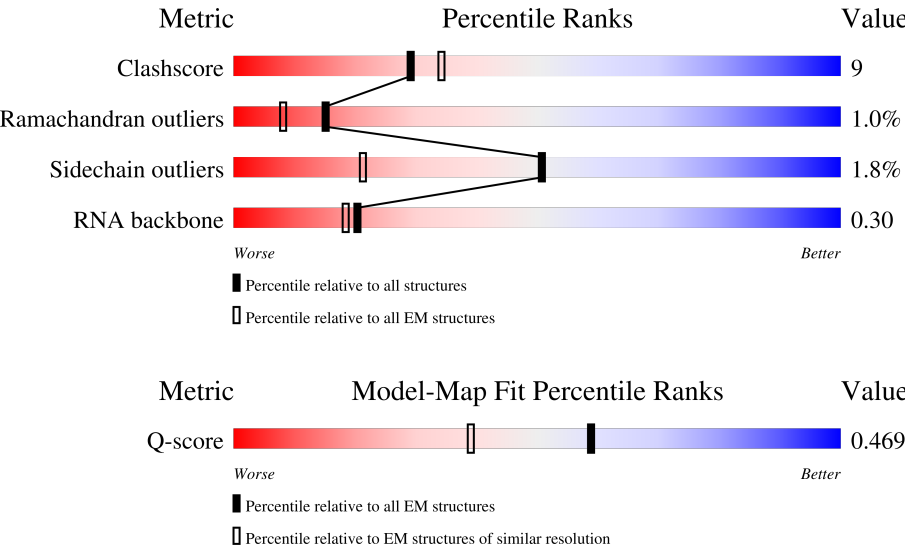
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



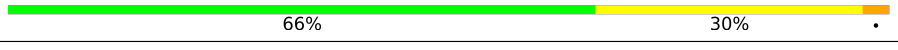
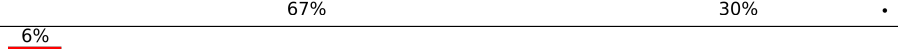
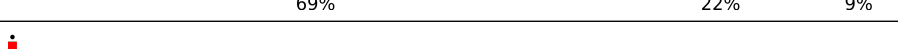
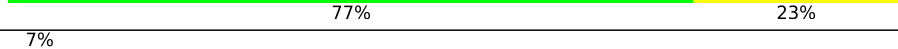
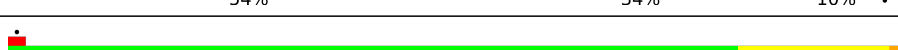
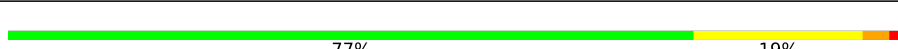
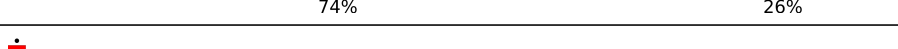
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	CO	205	
2	CL	210	
3	CV	134	

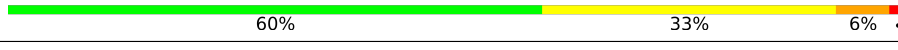
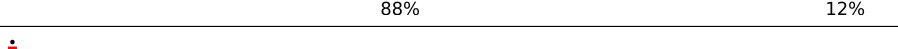
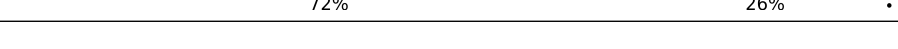
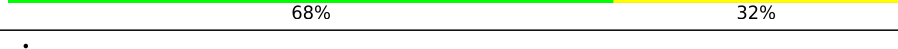
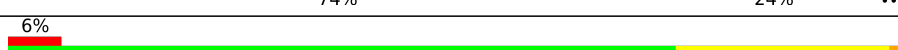
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Mol	Chain	Length	Quality of chain
4	CM	159	
5	Ca	149	
6	CN	203	
7	CI	217	
8	CD	290	
9	CQ	187	
10	CR	203	
11	CA	253	
12	CS	173	
13	CT	158	
14	CP	185	
15	CX	120	
16	CY	131	
17	CZ	134	
18	Cr	134	
19	Ch	123	
20	Cb	75	
21	CB	414	
22	CF	226	
23	Cc	100	
24	Ce	132	
25	Cf	157	
26	Ci	113	
27	Ck	70	
28	Cl	50	

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Mol	Chain	Length	Quality of chain
29	CC	392	
30	Cm	52	
31	Cn	25	
32	Cp	91	
33	Co	104	
34	CJ	182	
35	CH	190	
36	CE	228	
37	CG	241	
38	A9	30	
39	A7	120	
40	A8	123	
41	Ag	318	
42	AU	102	
43	AO	127	
44	AX	143	
45	AM	119	
46	Ad	52	
47	AN	150	
48	AL	155	
49	AR	120	
50	AP	124	
51	AB	220	
52	AA	218	
53	AV	82	

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Mol	Chain	Length	Quality of chain
54	AY	126	
55	AZ	74	
56	Aa	107	
57	Ab	84	
58	AD	227	
59	Ae	58	
60	Af	80	
61	AJ	181	
62	AE	261	
63	AC	227	
64	AG	231	
65	AH	194	
66	AI	207	
67	AQ	148	
68	Cz	217	
69	A5	3703	
70	B2	1936	
71	AW	129	
72	AT	126	
73	AK	90	
74	AF	189	
75	Ac	62	
76	CU	99	
77	Cj	87	
78	CW	60	

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Mol	Chain	Length	Quality of chain
79	Cg	103	 73% 22% 5%
80	Cd	107	 51% 43% 6%
81	AS	136	 18% 50% 50%

2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 216955 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CO	205	Total	C	N	O	S	0	0
			1668	1063	331	268	6		

- Molecule 2 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CL	210	Total	C	N	O	S	0	0
			1695	1066	342	284	3		

- Molecule 3 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CV	134	Total	C	N	O	S	0	0
			998	629	190	173	6		

- Molecule 4 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CM	159	Total	C	N	O	S	0	0
			1302	826	256	218	2		

- Molecule 5 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Ca	149	Total	C	N	O	S	0	0
			1204	769	242	189	4		

- Molecule 6 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CN	203	Total	C	N	O	S	0	0
			1710	1072	362	271	5		

- Molecule 7 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CI	217	Total	C	N	O	S	0	0
			1785	1125	343	304	13		

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CD	290	Total	C	N	O	S	0	0
			2334	1471	434	423	6		

- Molecule 9 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CQ	187	Total	C	N	O	S	0	0
			1518	957	306	251	4		

- Molecule 10 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CR	203	Total	C	N	O	S	0	0
			1683	1047	350	277	9		

- Molecule 11 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	CA	253	Total	C	N	O	S	0	0
			1935	1206	395	326	8		

- Molecule 12 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CS	173	Total	C	N	O	S	0	0
			1454	935	275	240	4		

- Molecule 13 is a protein called RE62581p.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CT	158	Total	C	N	O	S	0	0
			1297	829	253	212	3		

- Molecule 14 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	CP	185	Total	C	N	O	S	0	0
			1505	928	305	263	9		

- Molecule 15 is a protein called IP17216p.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	CX	120	Total	C	N	O	S	0	0
			984	625	192	165	2		

- Molecule 16 is a protein called GEO07453p1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	CY	131	Total	C	N	O	S	0	0
			1078	676	224	176	2		

- Molecule 17 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	CZ	134	Total	C	N	O	S	0	0
			1115	723	209	180	3		

- Molecule 18 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Cr	134	Total	C	N	O	0	0
			1051	670	205	176		

- Molecule 19 is a protein called FI02809p.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Ch	123	Total	C	N	O	S	0	0
			1015	646	202	164	3		

- Molecule 20 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Cb	75	Total	C	N	O	S	0	0
			619	378	133	107	1		

- Molecule 21 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CB	414	Total	C	N	O	S	0	0
			3287	2083	621	565	18		

- Molecule 22 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	CF	226	Total	C	N	O	S	0	0
			1895	1216	368	308	3		

- Molecule 23 is a protein called RE25263p.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Cc	100	Total	C	N	O	S	0	0
			770	486	132	147	5		

- Molecule 24 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Ce	132	Total	C	N	O	S	0	0
			1110	698	230	177	5		

- Molecule 25 is a protein called GEO07455p1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Cf	157	Total	C	N	O	S	0	0
			1244	781	255	203	5		

- Molecule 26 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Ci	113	Total	C	N	O	S	0	0
			934	585	193	153	3		

- Molecule 27 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Ck	70	Total	C	N	O	S	0	0
			576	366	108	100	2		

- Molecule 28 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	Cl	50	Total	C	N	O	0	0
			437	276	98	63		

- Molecule 29 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	CC	392	Total	C	N	O	S	0	0
			3109	1959	622	522	6		

- Molecule 30 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Cm	52	Total	C	N	O	S	0	0
			429	267	89	67	6		

- Molecule 31 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Cn	25	Total	C	N	O	S	0	0
			236	143	63	27	3		

- Molecule 32 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Cp	91	Total	C	N	O	S	0	0
			710	441	140	122	7		

- Molecule 33 is a protein called TA01007p.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Co	104	Total	C	N	O	S	0	0
			874	548	180	138	8		

- Molecule 34 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	CJ	182	Total	C	N	O	S	0	0
			1468	926	278	258	6		

- Molecule 35 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	CH	190	Total	C	N	O	S	0	0
			1499	947	265	278	9		

- Molecule 36 is a protein called Ribosomal protein L6, isoform A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	CE	228	Total	C	N	O	S	0	0
			1845	1185	351	305	4		

- Molecule 37 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	CG	241	Total	C	N	O	S	0	0
			1936	1237	368	327	4		

- Molecule 38 is a RNA chain called 2S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A9	30	Total	C	N	O	P	0	0
			639	286	111	213	29		

- Molecule 39 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	A7	120	Total	C	N	O	P	0	0
			2554	1141	456	838	119		

- Molecule 40 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A8	123	Total	C	N	O	P	0	0
			2621	1173	474	852	122		

- Molecule 41 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Ag	318	Total	C	N	O	S	0	0
			2511	1577	444	480	10		

- Molecule 42 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AU	102	Total	C	N	O	S	0	0
			815	505	161	145	4		

- Molecule 43 is a protein called 40S ribosomal protein S14a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AO	127	Total	C	N	O	S	0	0
			953	587	185	177	4		

- Molecule 44 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AX	143	Total	C	N	O	S	0	0
			1131	712	226	191	2		

- Molecule 45 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AM	119	Total	C	N	O	S	0	0
			924	582	165	171	6		

- Molecule 46 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ad	52	Total	C	N	O	S	0	0
			433	269	87	72	5		

- Molecule 47 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	AN	150	Total	C	N	O	S	0	0
			1202	767	229	203	3		

- Molecule 48 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AL	155	Total	C	N	O	S	0	0
			1274	803	254	211	6		

- Molecule 49 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	AR	120	Total	C	N	O	S	0	0
			981	618	183	176	4		

- Molecule 50 is a protein called GEO07301p1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	AP	124	Total	C	N	O	S	0	0
			1016	652	189	169	6		

- Molecule 51 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AB	220	Total	C	N	O	S	0	0
			1798	1138	328	324	8		

- Molecule 52 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AA	218	Total	C	N	O	S	0	0
			1737	1113	298	321	5		

- Molecule 53 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	AV	82	Total	C	N	O	S	0	0
			617	373	114	125	5		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AV	2	GLN	GLU	conflict	UNP O76927
AV	8	PHE	ASN	conflict	UNP O76927
AV	25	GLY	HIS	conflict	UNP O76927
AV	32	ILE	VAL	conflict	UNP O76927
AV	34	MET	LEU	conflict	UNP O76927
AV	35	ASN	SER	conflict	UNP O76927
AV	36	VAL	ILE	conflict	UNP O76927
AV	58	ALA	GLU	conflict	UNP O76927
AV	68	SER	CYS	conflict	UNP O76927
AV	70	LEU	VAL	conflict	UNP O76927
AV	75	ALA	LYS	conflict	UNP O76927
AV	79	VAL	ILE	conflict	UNP O76927

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Chain	Residue	Modelled	Actual	Comment	Reference
AV	80	SER	THR	conflict	UNP O76927

- Molecule 54 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AY	126	Total	C	N	O	S	0	0
			1016	644	196	171	5		

- Molecule 55 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AZ	74	Total	C	N	O	S	0	0
			608	390	112	106			

- Molecule 56 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Aa	107	Total	C	N	O	S	0	0
			867	539	182	140	6		

- Molecule 57 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Ab	84	Total	C	N	O	S	0	0
			653	412	123	110	8		

- Molecule 58 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AD	227	Total	C	N	O	S	0	0
			1782	1127	319	326	10		

- Molecule 59 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Ae	58	Total	C	N	O	S	0	0
			469	289	105	75			

- Molecule 60 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Af	80	Total	C	N	O	S	0	0
			659	417	128	109	5		

- Molecule 61 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AJ	181	Total	C	N	O	S	0	0
			1503	957	298	247	1		

- Molecule 62 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AE	261	Total	C	N	O	S	0	0
			2054	1314	380	353	7		

- Molecule 63 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AC	227	Total	C	N	O	S	0	0
			1746	1126	302	311	7		

- Molecule 64 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AG	231	Total	C	N	O	S	0	0
			1866	1172	372	315	7		

- Molecule 65 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AH	194	Total	C	N	O	S	0	0
			1566	1006	278	281	1		

- Molecule 66 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AI	207	Total	C	N	O	S	0	0
			1665	1037	329	296	3		

- Molecule 67 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AQ	148	Total	C	N	O	S	0	0
			1183	753	223	204	3		

- Molecule 68 is a protein called 60S ribosomal protein L10a-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Cz	217	Total	C	N	O	S	0	0
			1702	1084	303	305	10		

- Molecule 69 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	A5	3703	Total	C	N	O	P	0	0
			77093	34436	13555	25401	3701		

- Molecule 70 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	B2	1936	Total	C	N	O	P	0	0
			39355	17526	6780	13114	1935		

- Molecule 71 is a protein called 40S ribosomal protein S15Aa.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AW	129	Total	C	N	O	S	0	0
			1028	656	189	176	7		

- Molecule 72 is a protein called 40S ribosomal protein S19a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AT	126	Total	C	N	O	S	0	0
			1000	635	192	170	3		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AT	?	-	GLU	deletion	UNP P39018
AT	?	-	HIS	deletion	UNP P39018
AT	?	-	ALA	deletion	UNP P39018
AT	?	-	ARG	deletion	UNP P39018
AT	?	-	LEU	deletion	UNP P39018
AT	?	-	VAL	deletion	UNP P39018

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Chain	Residue	Modelled	Actual	Comment	Reference
AT	?	-	GLU	deletion	UNP P39018
AT	?	-	LYS	deletion	UNP P39018
AT	?	-	HIS	deletion	UNP P39018
AT	?	-	PRO	deletion	UNP P39018
AT	?	-	ASP	deletion	UNP P39018
AT	?	-	GLY	deletion	UNP P39018
AT	?	-	GLY	deletion	UNP P39018

- Molecule 73 is a protein called 40S ribosomal protein S10b.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AK	90	Total	C	N	O	S	0	0
			760	500	130	127	3		

- Molecule 74 is a protein called 40S ribosomal protein S5b.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AF	189	Total	C	N	O	S	0	0
			1481	925	283	266	7		

- Molecule 75 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Ac	62	Total	C	N	O	S	0	0
			498	307	100	89	2		

- Molecule 76 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	CU	99	Total	C	N	O	S	0	0
			825	530	144	149	2		

- Molecule 77 is a protein called Probable 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Cj	87	Total	C	N	O	S	0	0
			704	430	154	115	5		

- Molecule 78 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	CW	60	Total	C	N	O	S	0	0
			503	326	95	78	4		

- Molecule 79 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Cg	103	Total	C	N	O	S	0	0
			844	525	176	138	5		

- Molecule 80 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Cd	107	Total	C	N	O	S	0	0
			893	556	176	159	2		

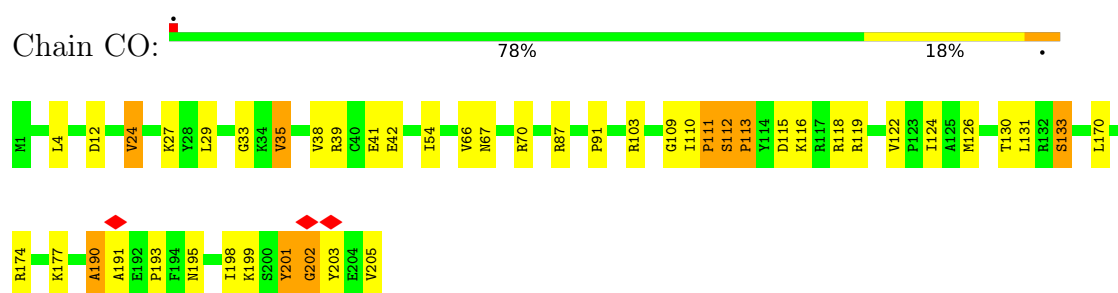
- Molecule 81 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	AS	136	Total	C	N	O	S	0	0
			1117	701	216	197	3		

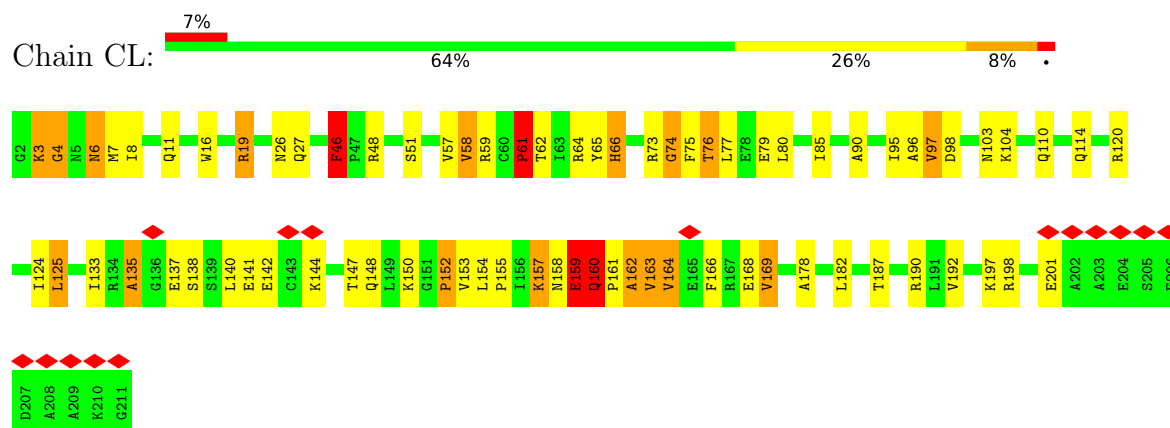
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

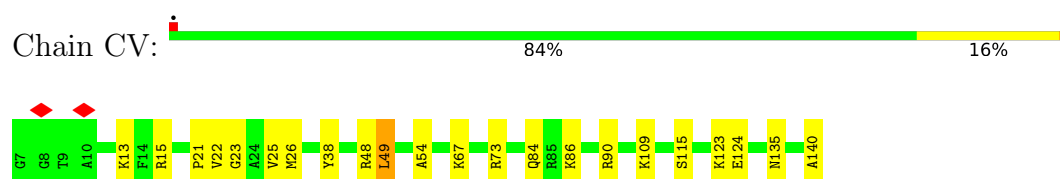
- Molecule 1: 60S ribosomal protein L13a



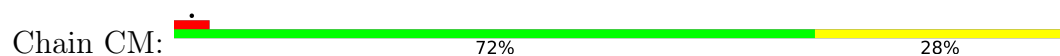
- Molecule 2: 60S ribosomal protein L13

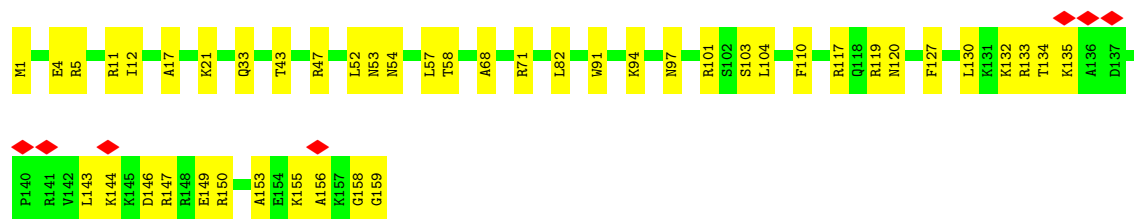


- Molecule 3: 60S ribosomal protein L23

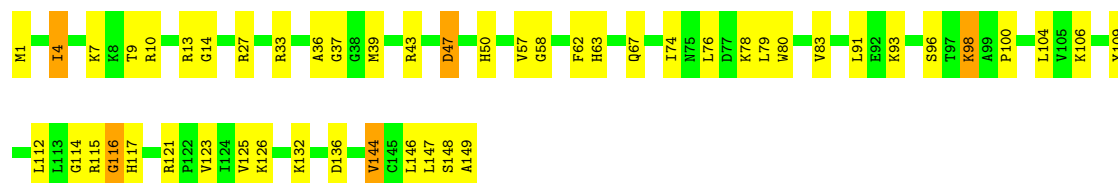


- Molecule 4: 60S ribosomal protein L14

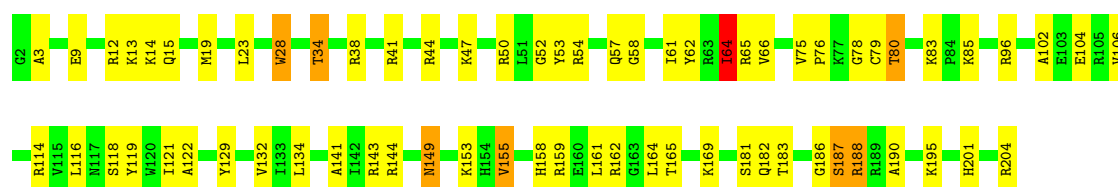




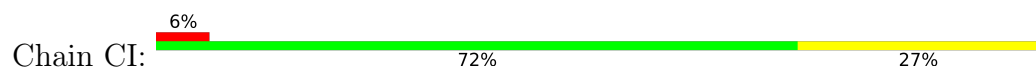
• Molecule 5: 60S ribosomal protein L27a



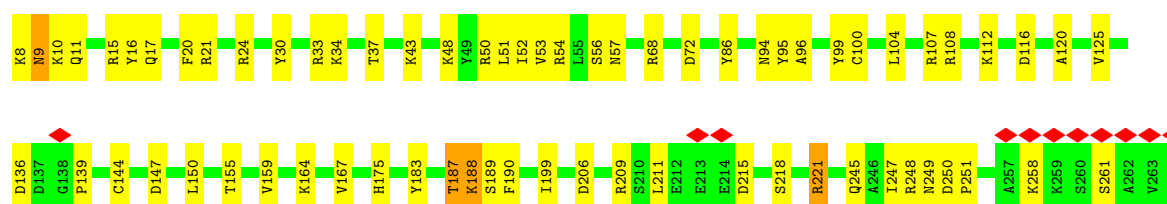
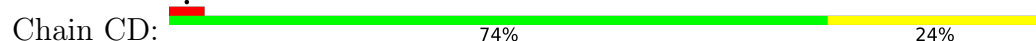
• Molecule 6: 60S ribosomal protein L15



• Molecule 7: 60S ribosomal protein L10



• Molecule 8: 60S ribosomal protein L5





- Molecule 9: 60S ribosomal protein L18

Chain CQ: 68% 29% ..



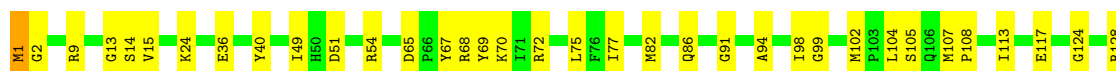
- Molecule 10: 60S ribosomal protein L19

Chain CR: 12% 77% 21% .



- Molecule 11: 60S ribosomal protein L8

Chain CA: 72% 27% .

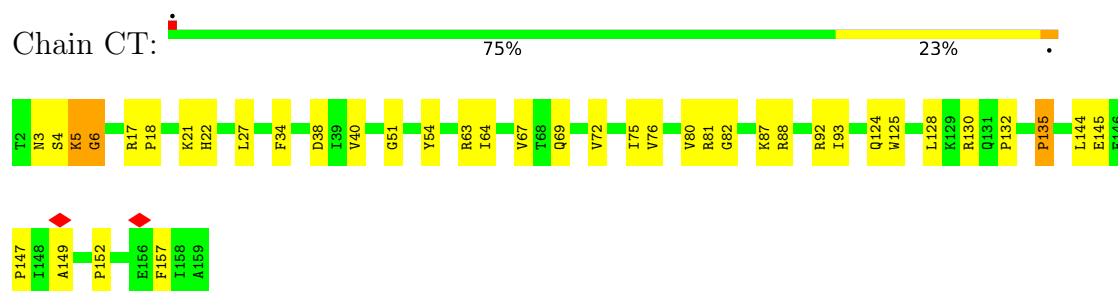


- Molecule 12: 60S ribosomal protein L18a

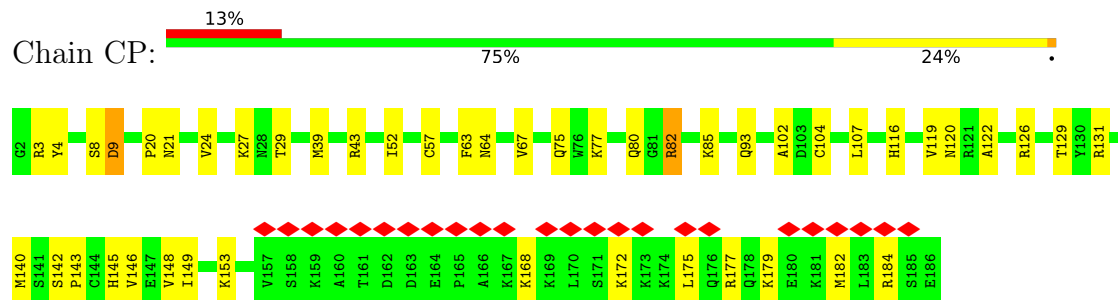
Chain CS: 69% 22% 9% .



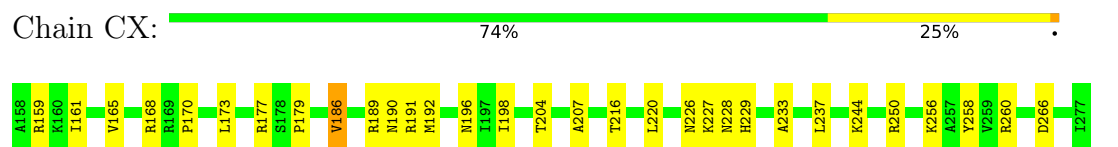
- Molecule 13: RE62581p



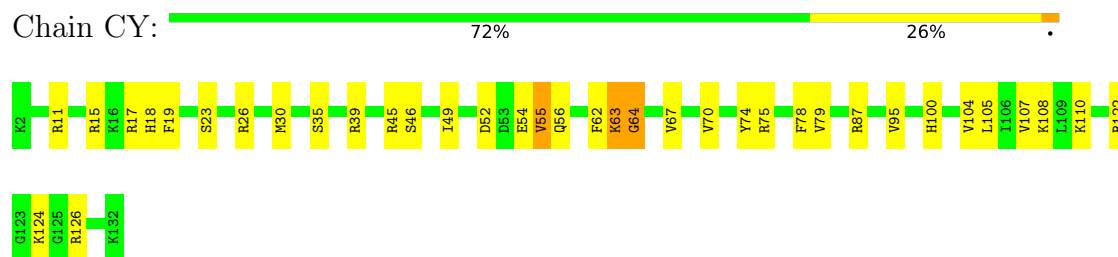
- Molecule 14: 60S ribosomal protein L17



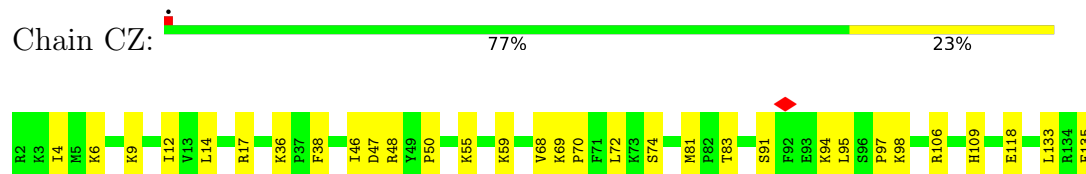
- Molecule 15: IP17216p



- Molecule 16: GEO07453p1

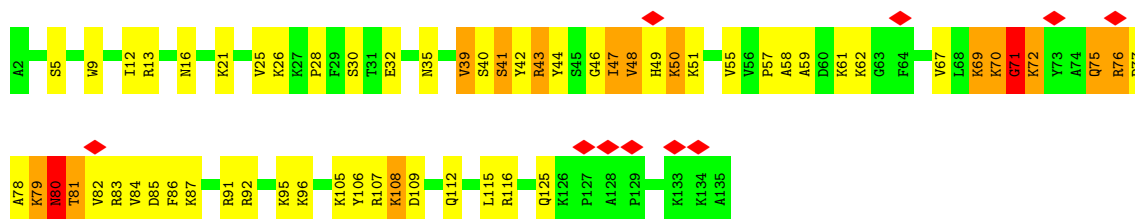


- Molecule 17: 60S ribosomal protein L27

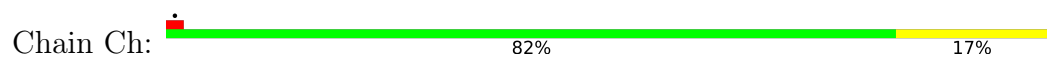


- Molecule 18: 60S ribosomal protein L28

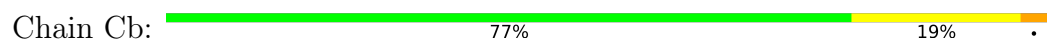




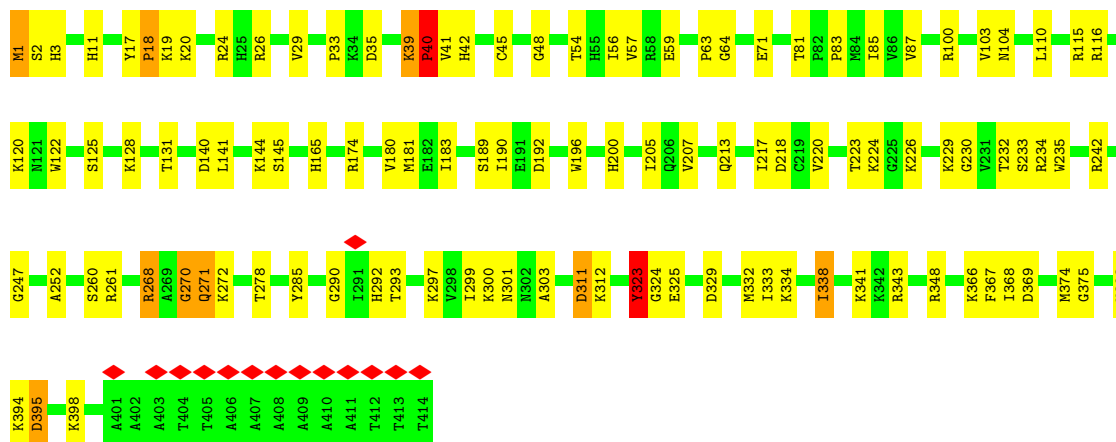
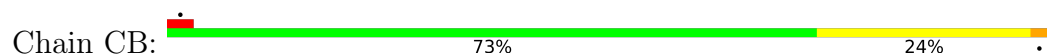
• Molecule 19: FI02809p



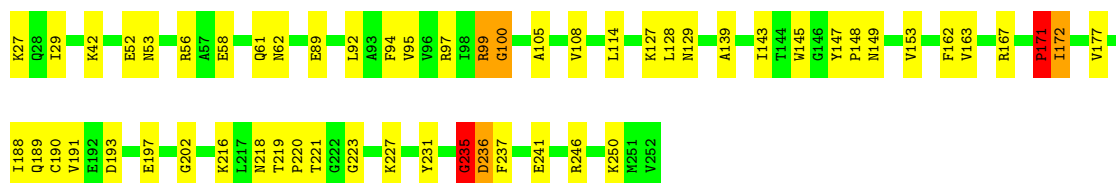
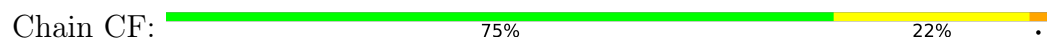
• Molecule 20: 60S ribosomal protein L29



• Molecule 21: 60S ribosomal protein L3



• Molecule 22: 60S ribosomal protein L7



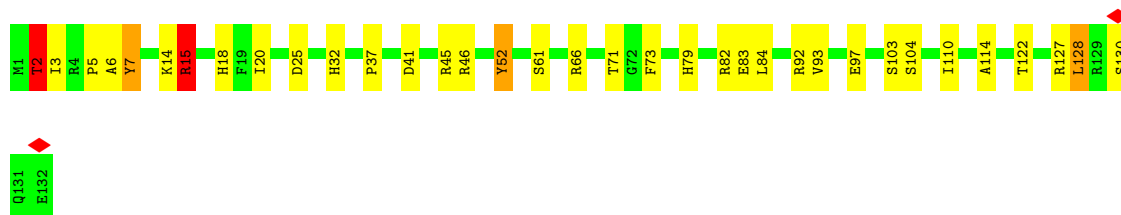
• Molecule 23: RE25263p

Chain Cc:  74% 26%



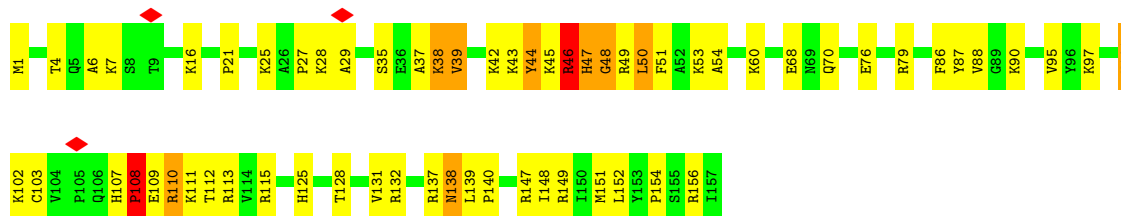
- Molecule 24: 60S ribosomal protein L32

Chain Ce:  73% 23%



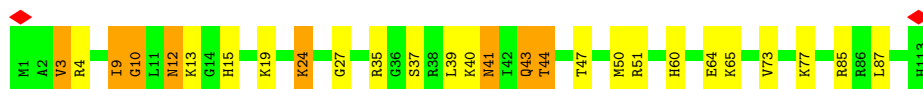
- Molecule 25: GEO07455p1

Chain Cf:  60% 33% 6%



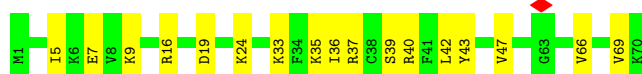
- Molecule 26: 60S ribosomal protein L36

Chain Ci:  76% 17% 7%



- Molecule 27: 60S ribosomal protein L38

Chain Ck:  76% 24%

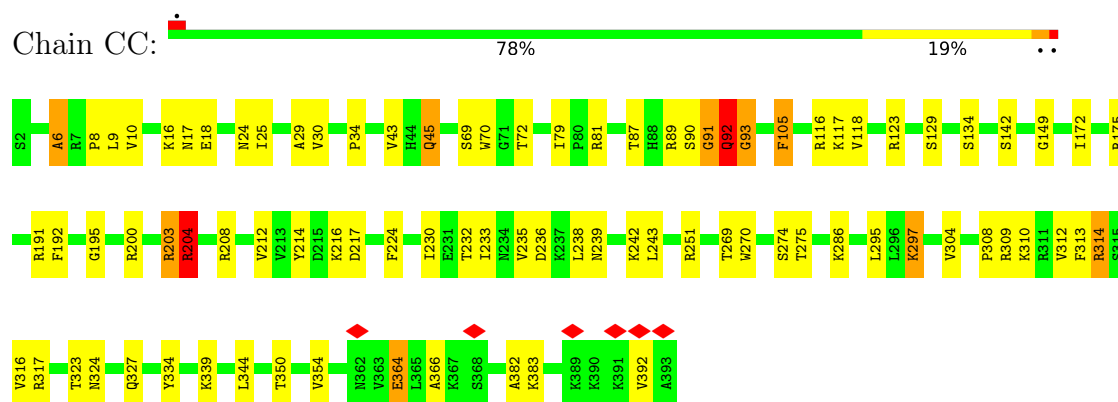


- Molecule 28: 60S ribosomal protein L39

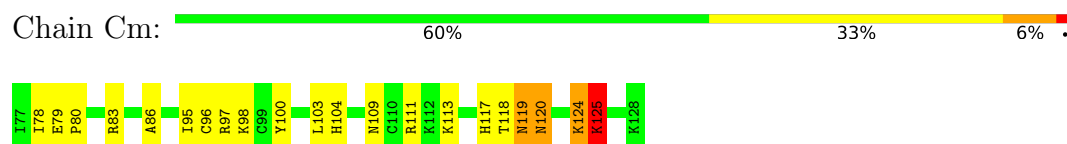
Chain Cl:  86% 14%



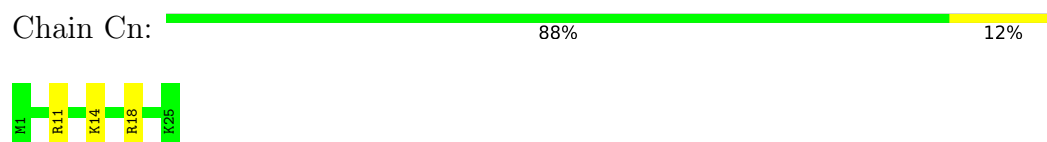
- Molecule 29: 60S ribosomal protein L4



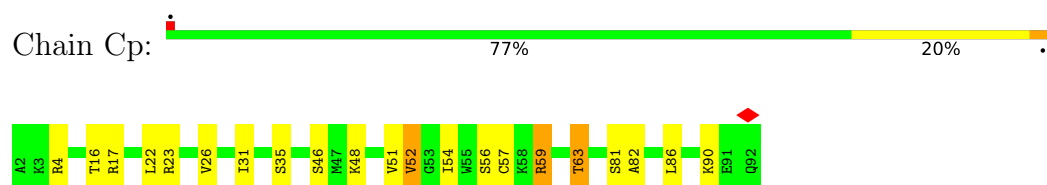
- Molecule 30: Ubiquitin-60S ribosomal protein L40



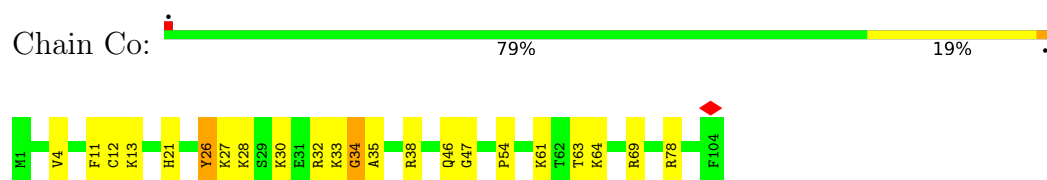
- Molecule 31: 60S ribosomal protein L41



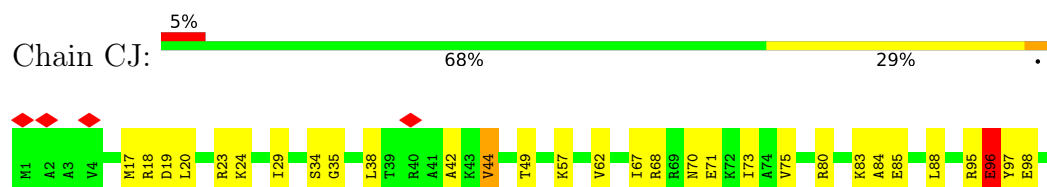
- Molecule 32: 60S ribosomal protein L37a

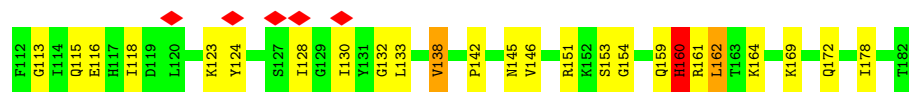


- Molecule 33: TA01007p



- Molecule 34: 60S ribosomal protein L11

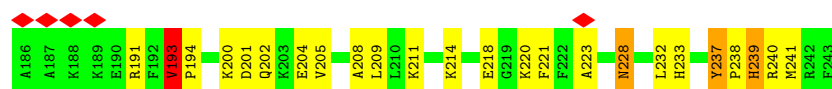
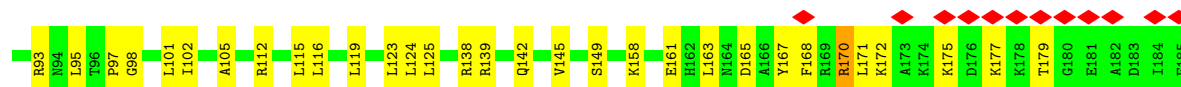
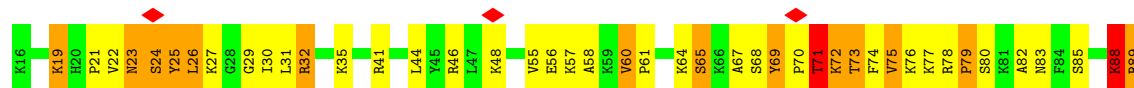




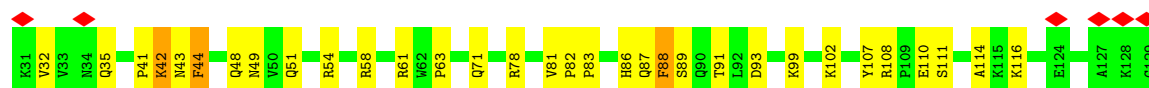
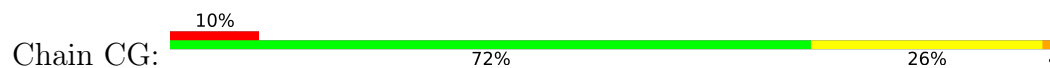
- Molecule 35: 60S ribosomal protein L9



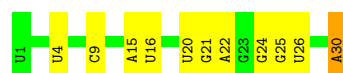
- Molecule 36: Ribosomal protein L6, isoform A



- Molecule 37: 60S ribosomal protein L7a

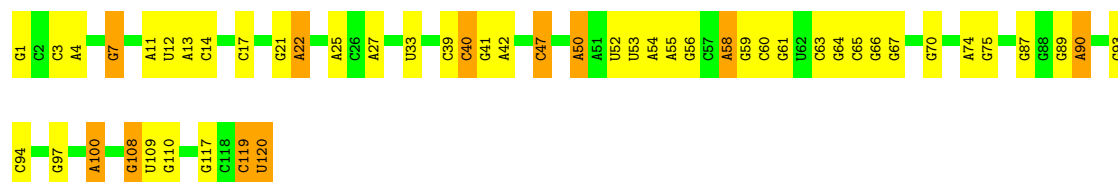


- Molecule 38: 2S ribosomal RNA



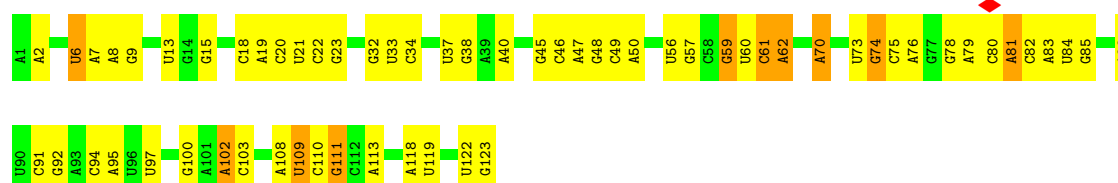
- Molecule 39: 5S ribosomal RNA

Chain A7: 



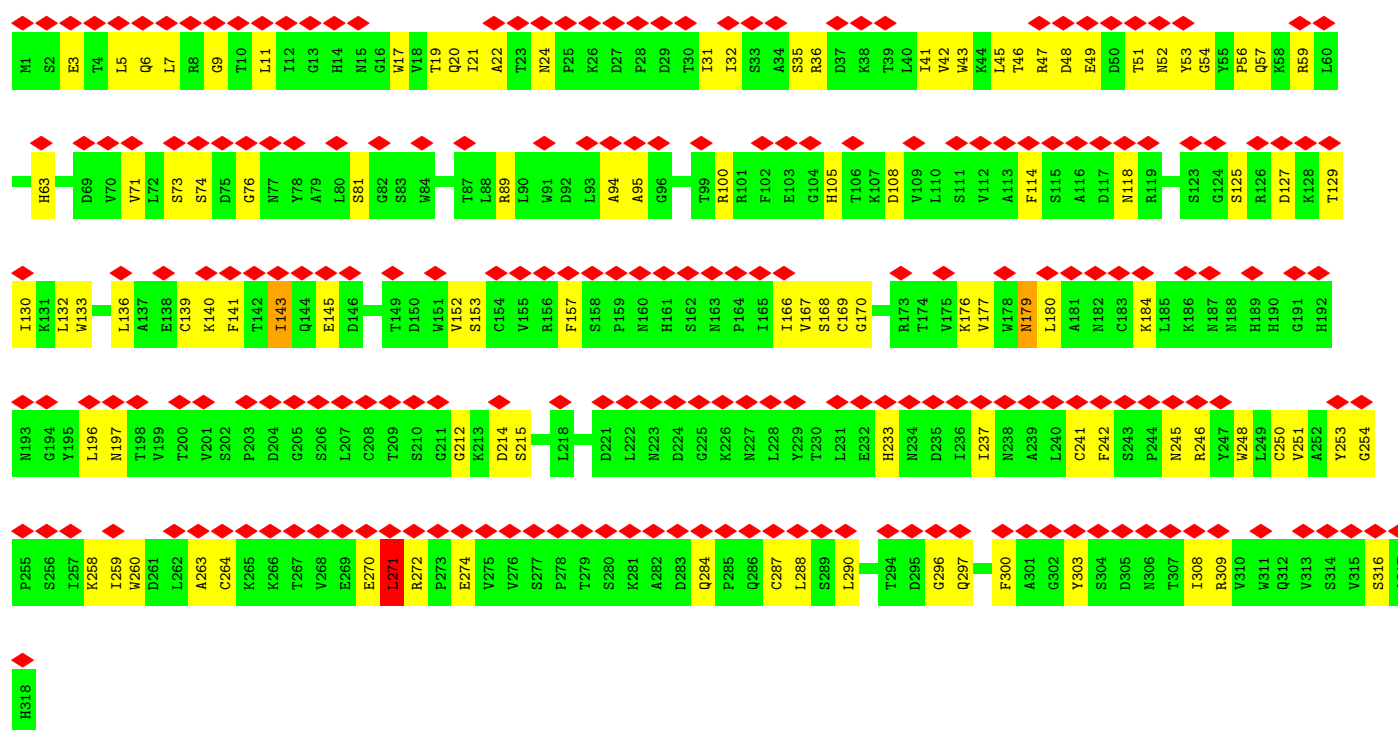
- Molecule 40: 5.8S ribosomal RNA

Chain A8: 



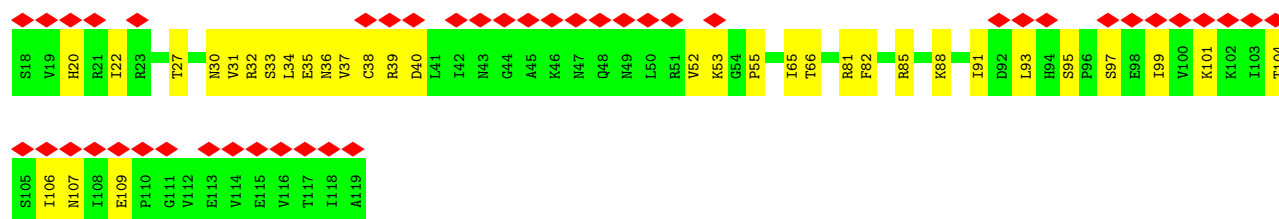
- Molecule 41: Guanine nucleotide-binding protein subunit beta-like protein

Chain Ag: 

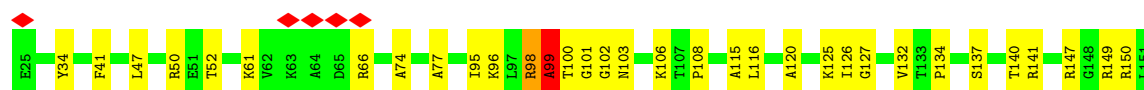
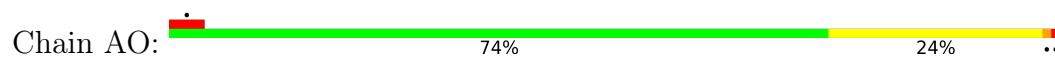


- Molecule 42: 40S ribosomal protein S20

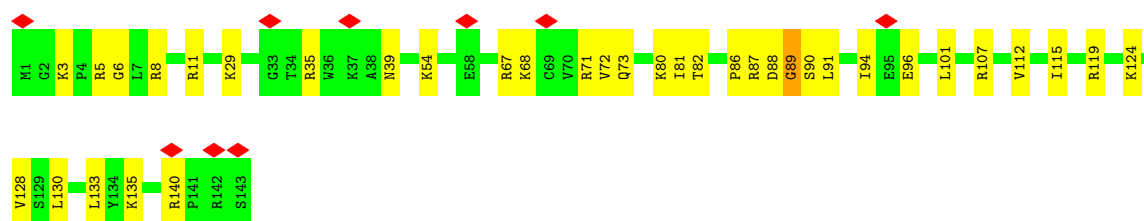
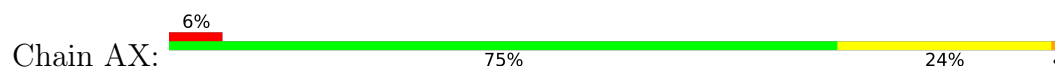
Chain AU: 



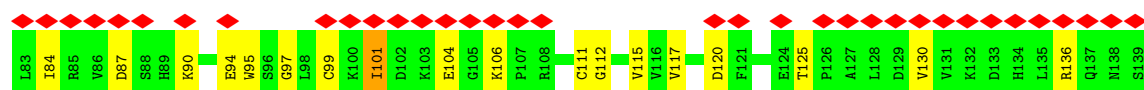
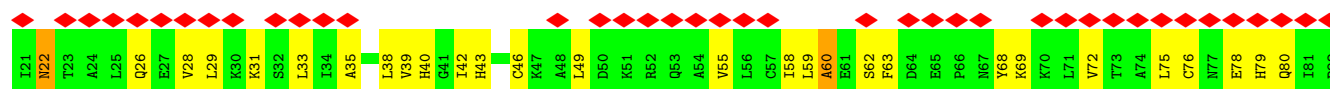
- Molecule 43: 40S ribosomal protein S14a



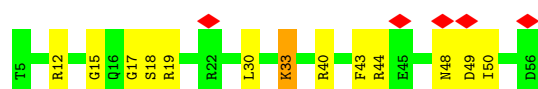
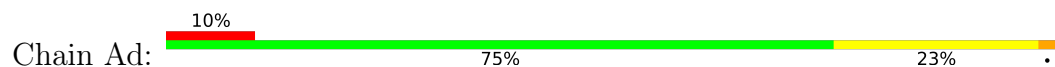
- Molecule 44: 40S ribosomal protein S23



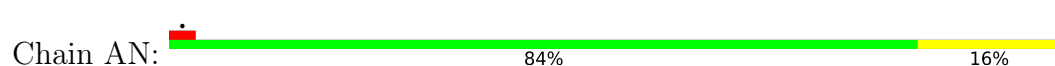
- Molecule 45: 40S ribosomal protein S12



- Molecule 46: 40S ribosomal protein S29

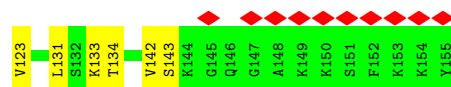
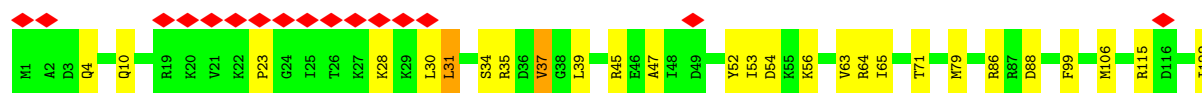
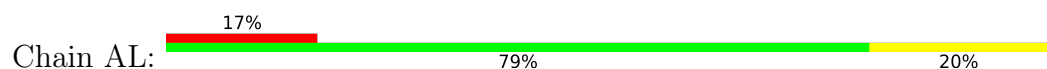


- Molecule 47: 40S ribosomal protein S13

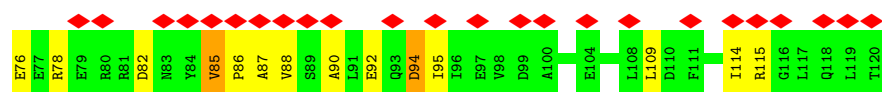
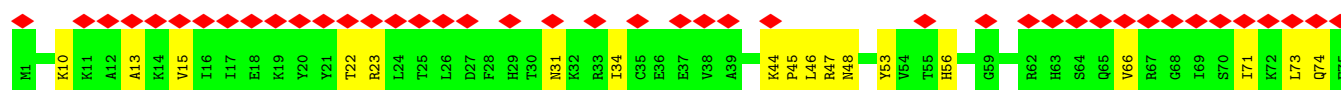
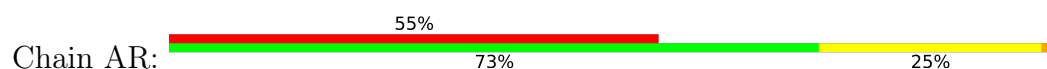




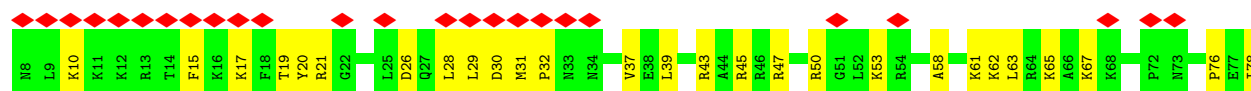
- Molecule 48: 40S ribosomal protein S11



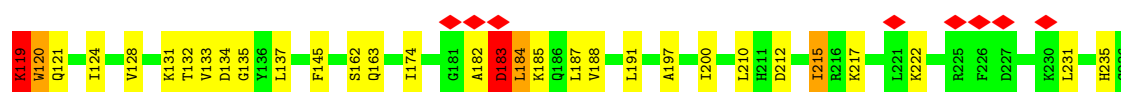
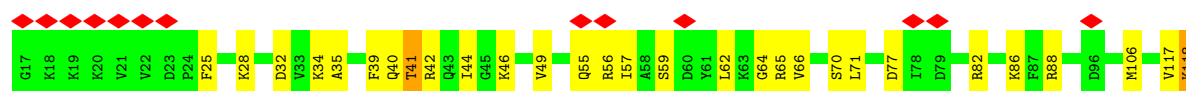
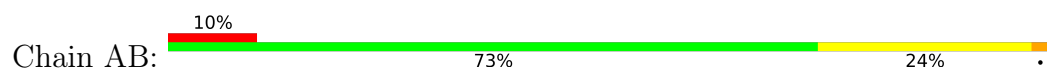
- Molecule 49: 40S ribosomal protein S17



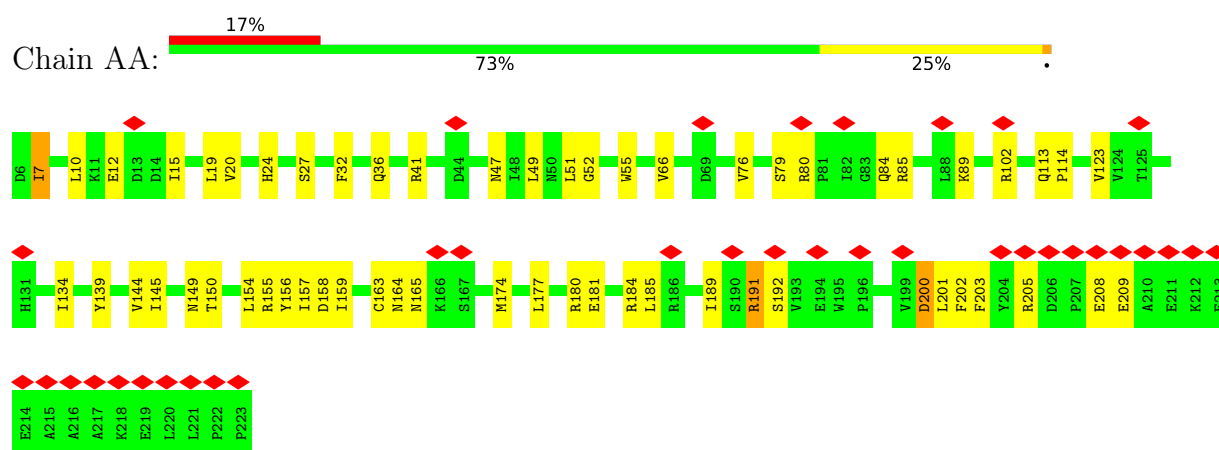
- Molecule 50: GEO07301p1



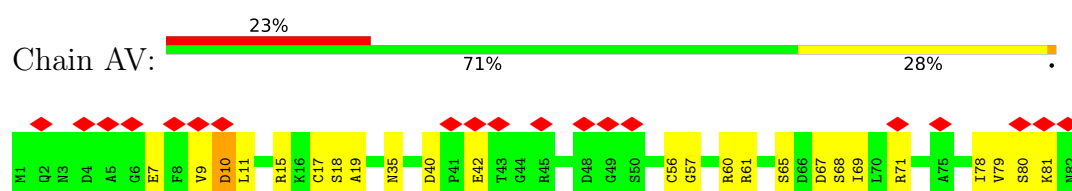
- Molecule 51: 40S ribosomal protein S3a



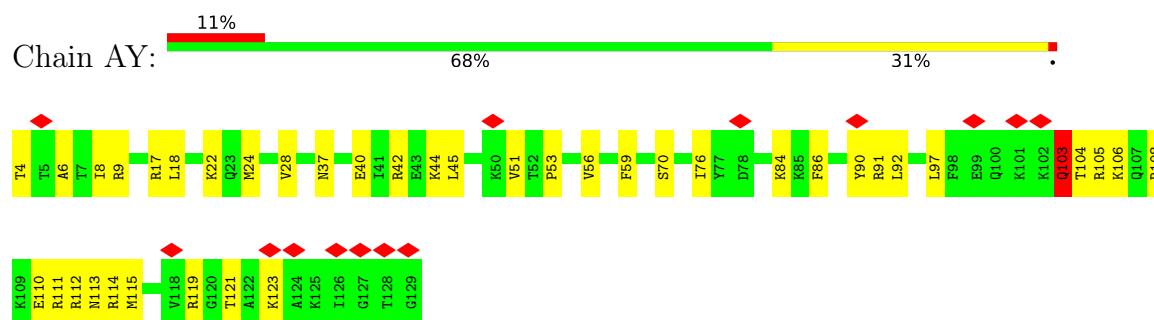
- Molecule 52: 40S ribosomal protein SA



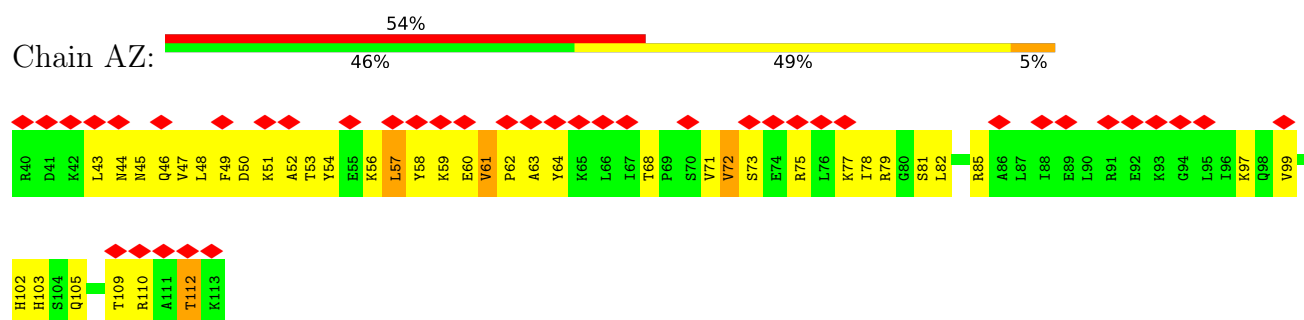
• Molecule 53: 40S ribosomal protein S21



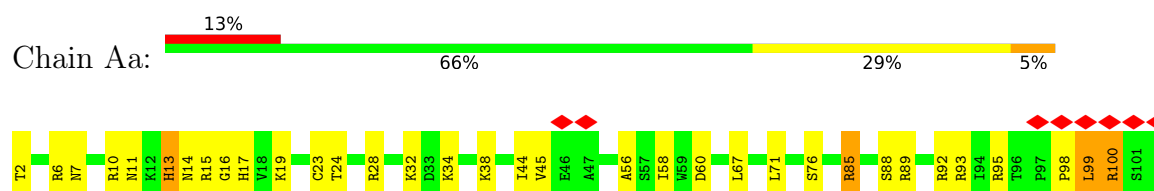
• Molecule 54: 40S ribosomal protein S24



• Molecule 55: 40S ribosomal protein S25

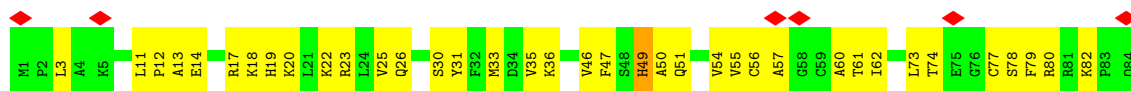


• Molecule 56: 40S ribosomal protein S26

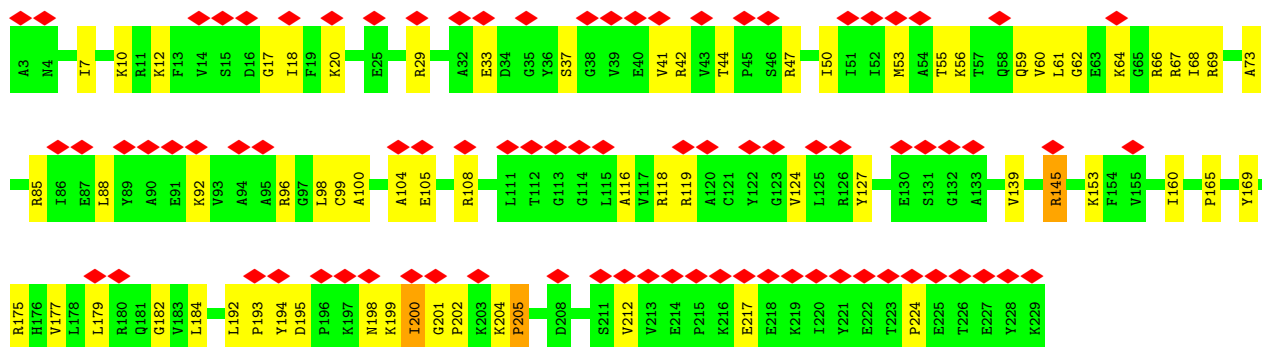
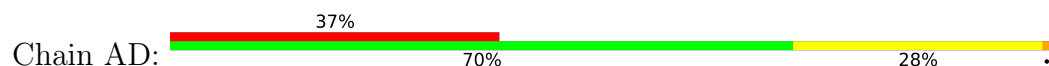




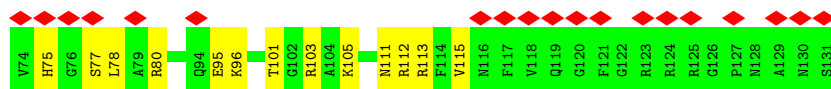
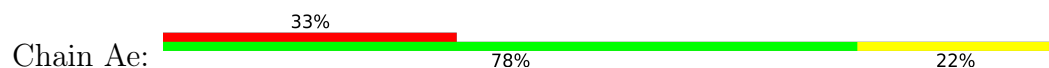
- Molecule 57: 40S ribosomal protein S27



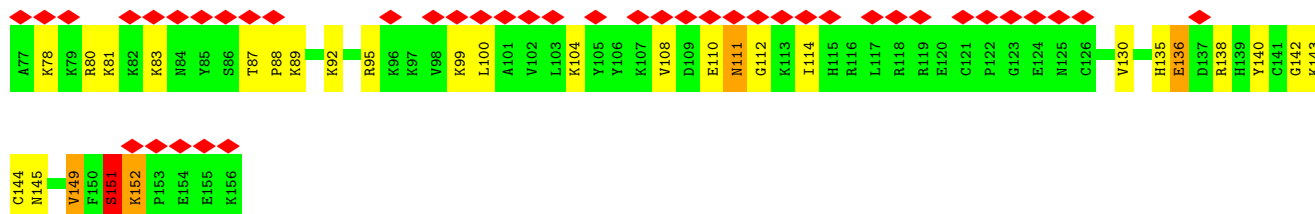
- Molecule 58: 40S ribosomal protein S3



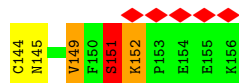
- Molecule 59: 40S ribosomal protein S30

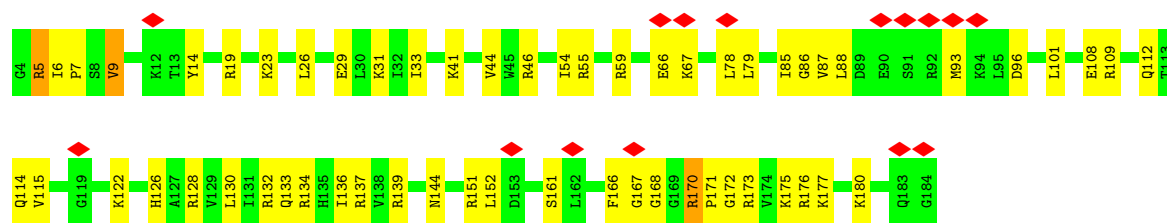


- Molecule 60: Ubiquitin-40S ribosomal protein S27a

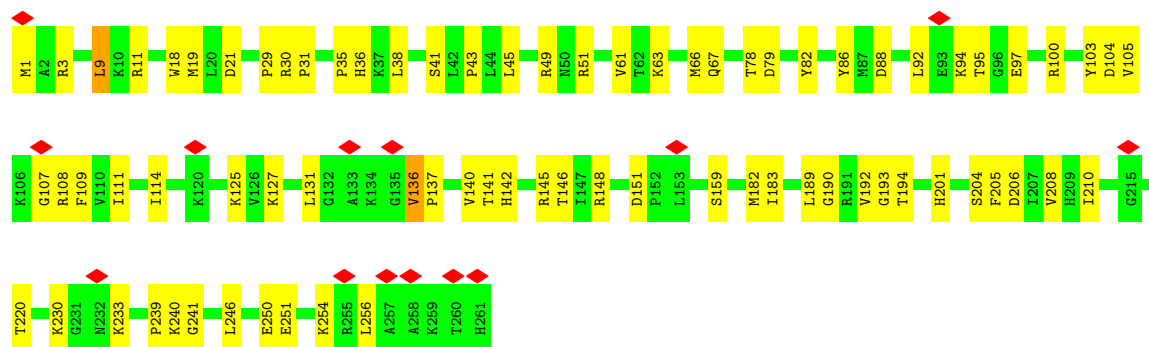
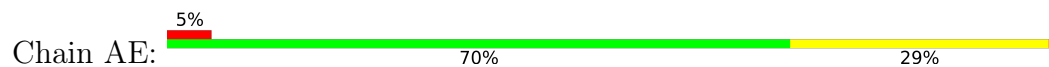


- Molecule 61: 40S ribosomal protein S9

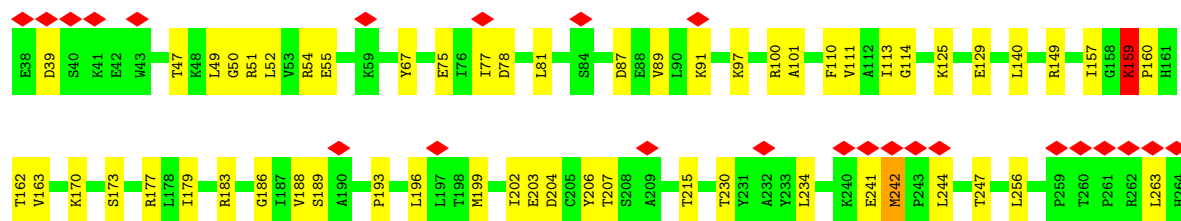
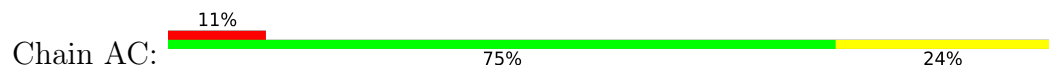




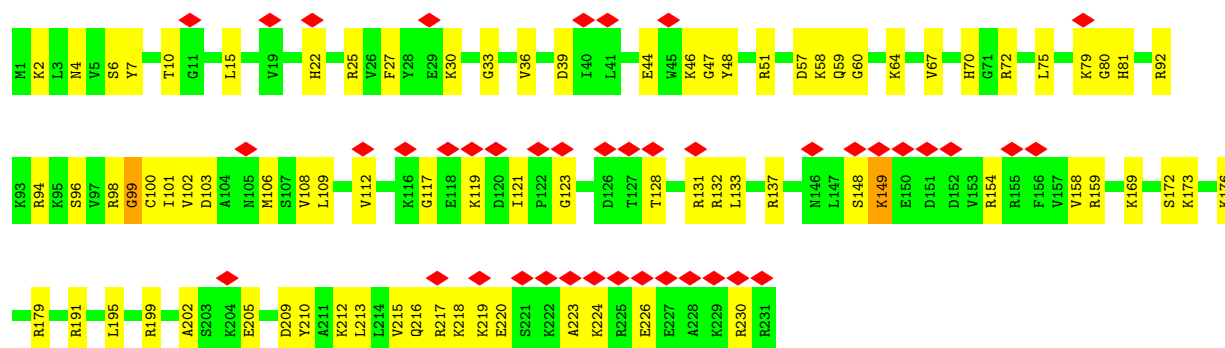
• Molecule 62: 40S ribosomal protein S4



• Molecule 63: 40S ribosomal protein S2

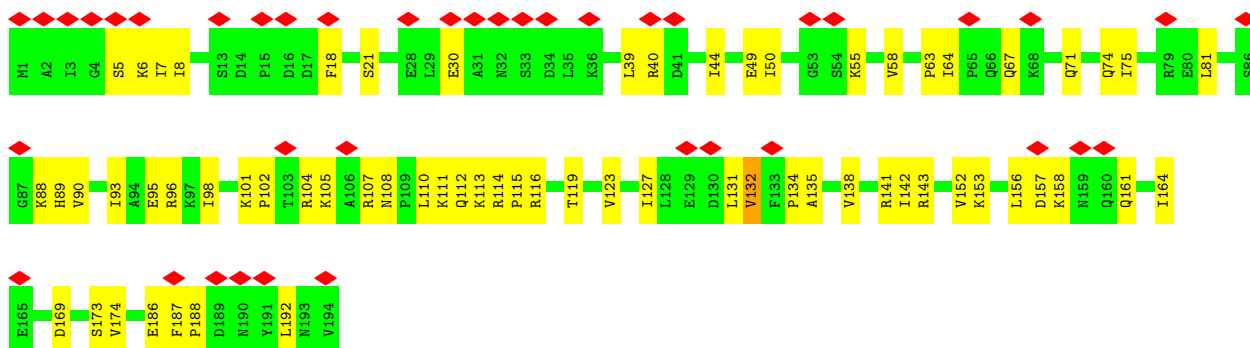


• Molecule 64: 40S ribosomal protein S6



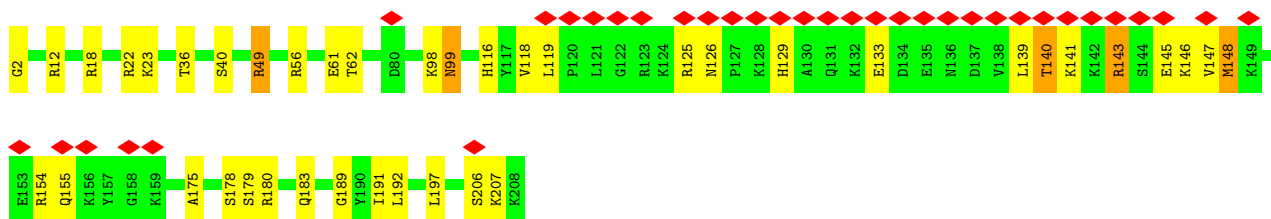
• Molecule 65: 40S ribosomal protein S7

Chain AH: 21% 66% 34%



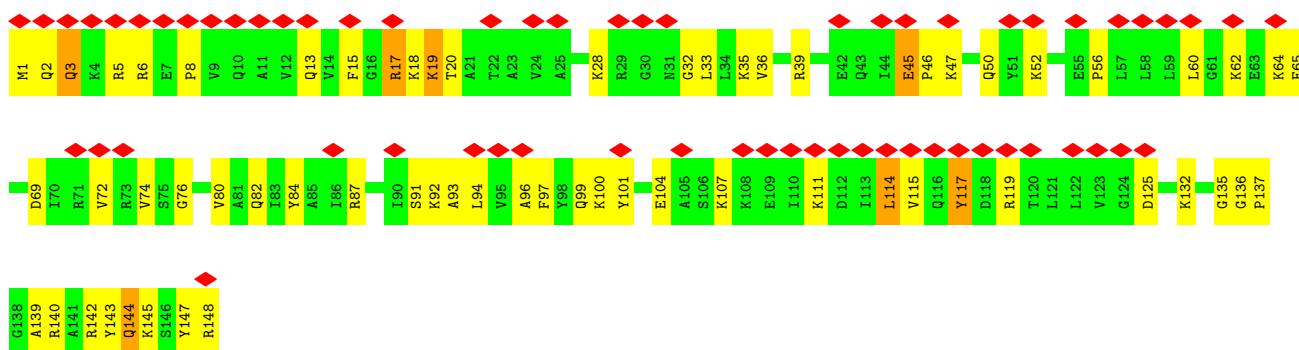
- Molecule 66: 40S ribosomal protein S8

Chain AI: 17% 80% 17%



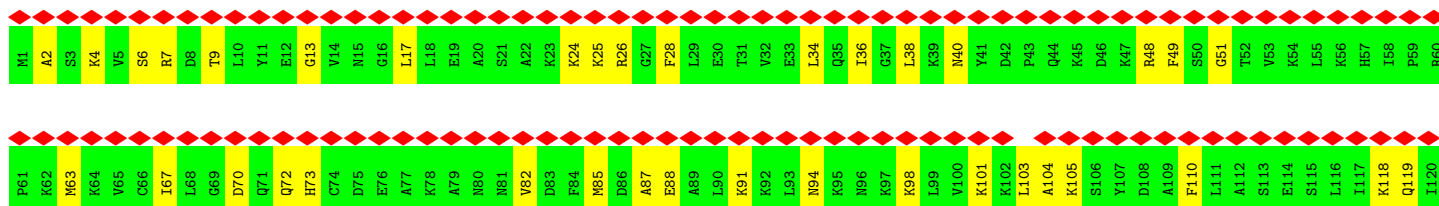
- Molecule 67: 40S ribosomal protein S16

Chain AQ: 42% 56% 39% 5%



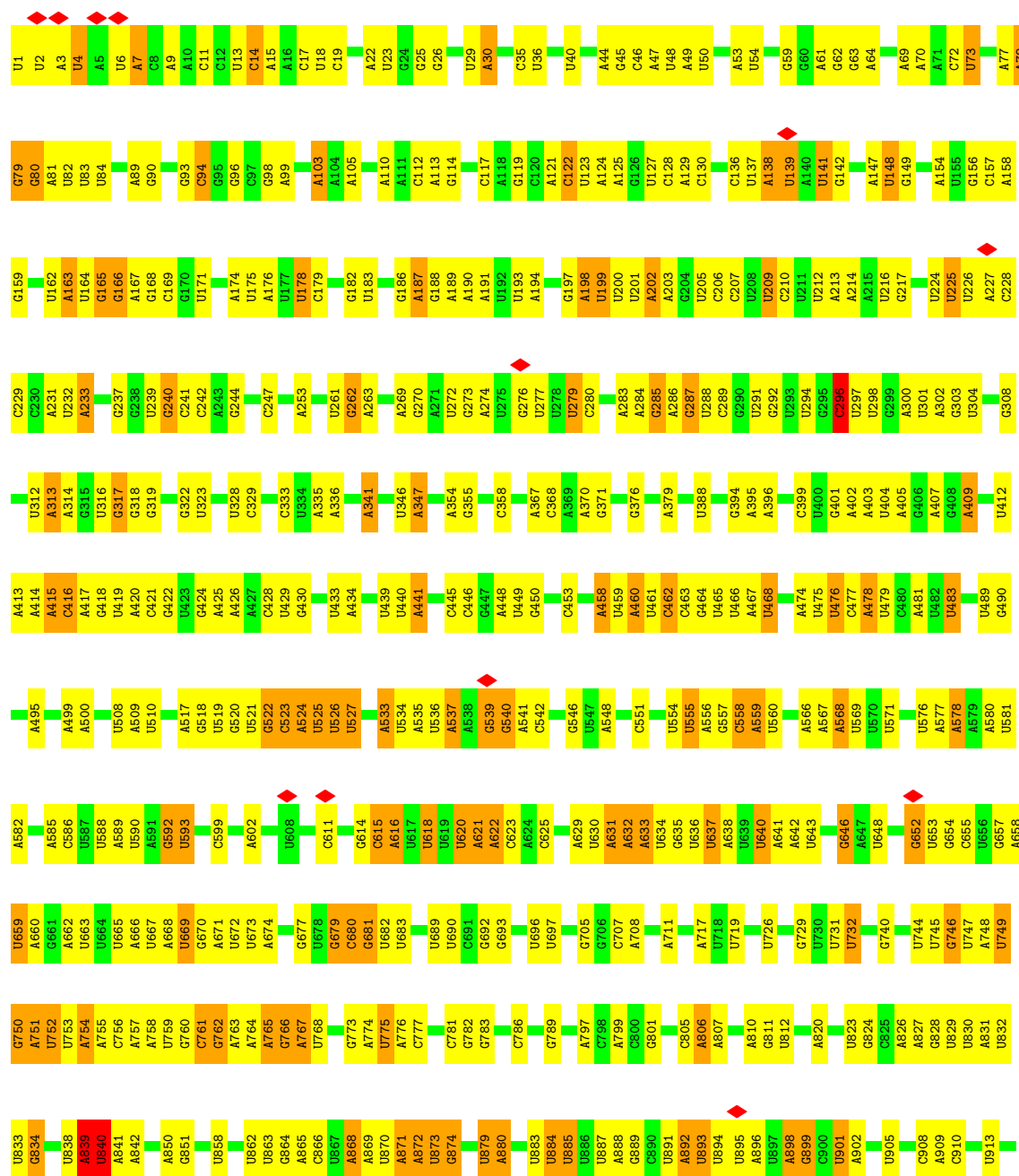
- Molecule 68: 60S ribosomal protein L10a-2

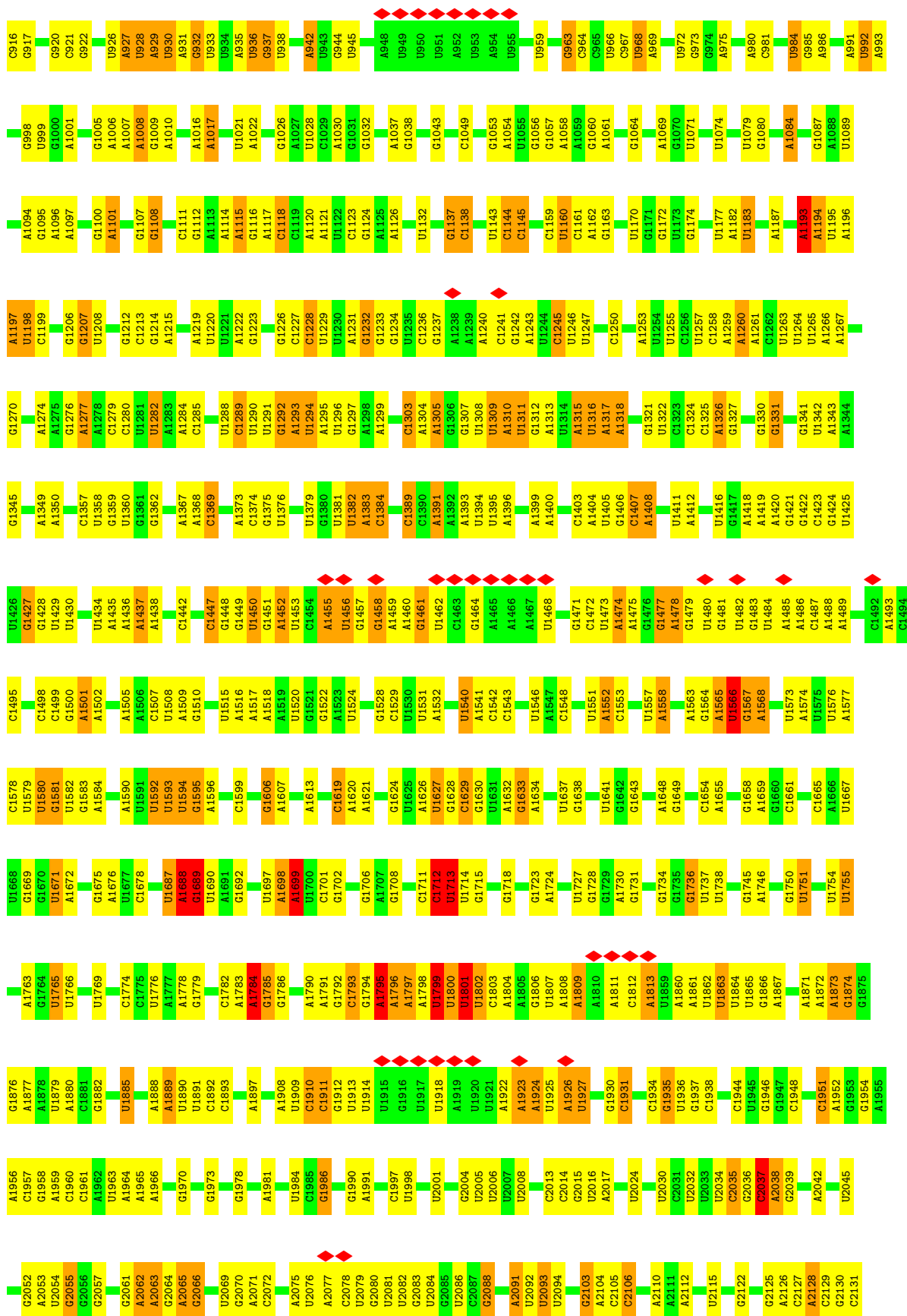
Chain Cz: 99% 70% 30%



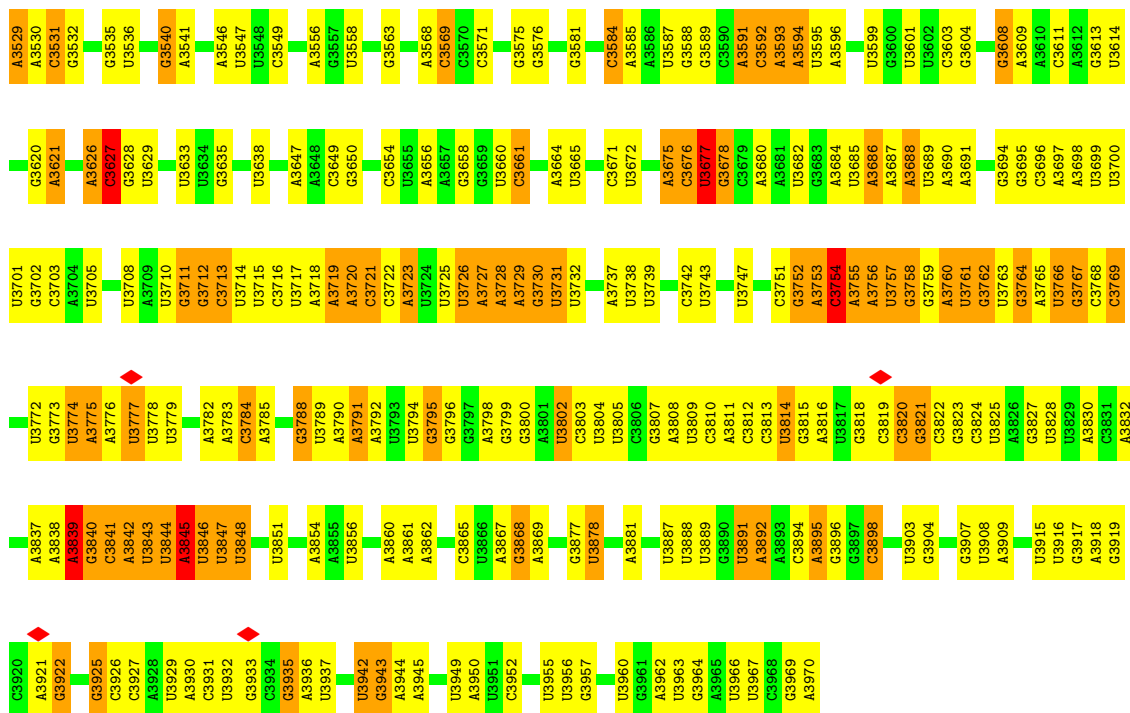


• Molecule 69: 28S ribosomal RNA

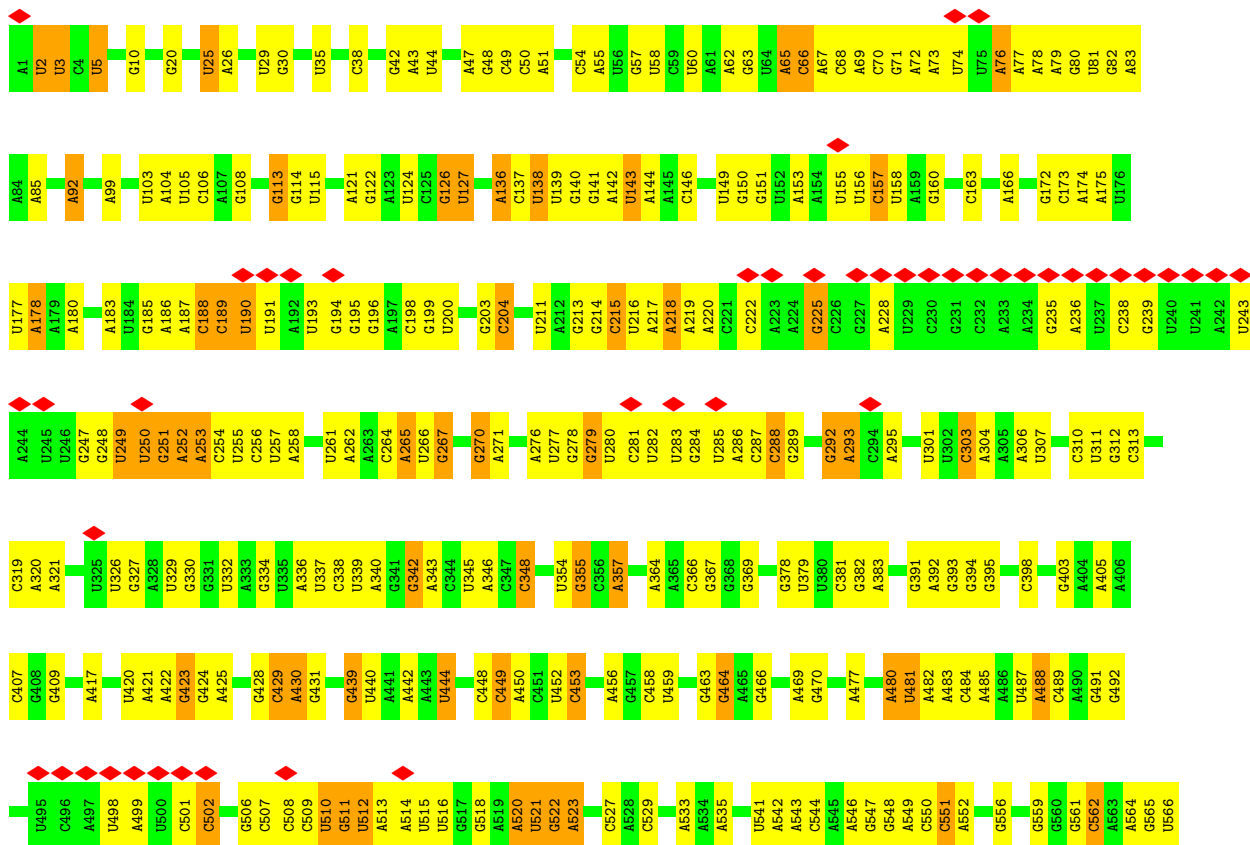


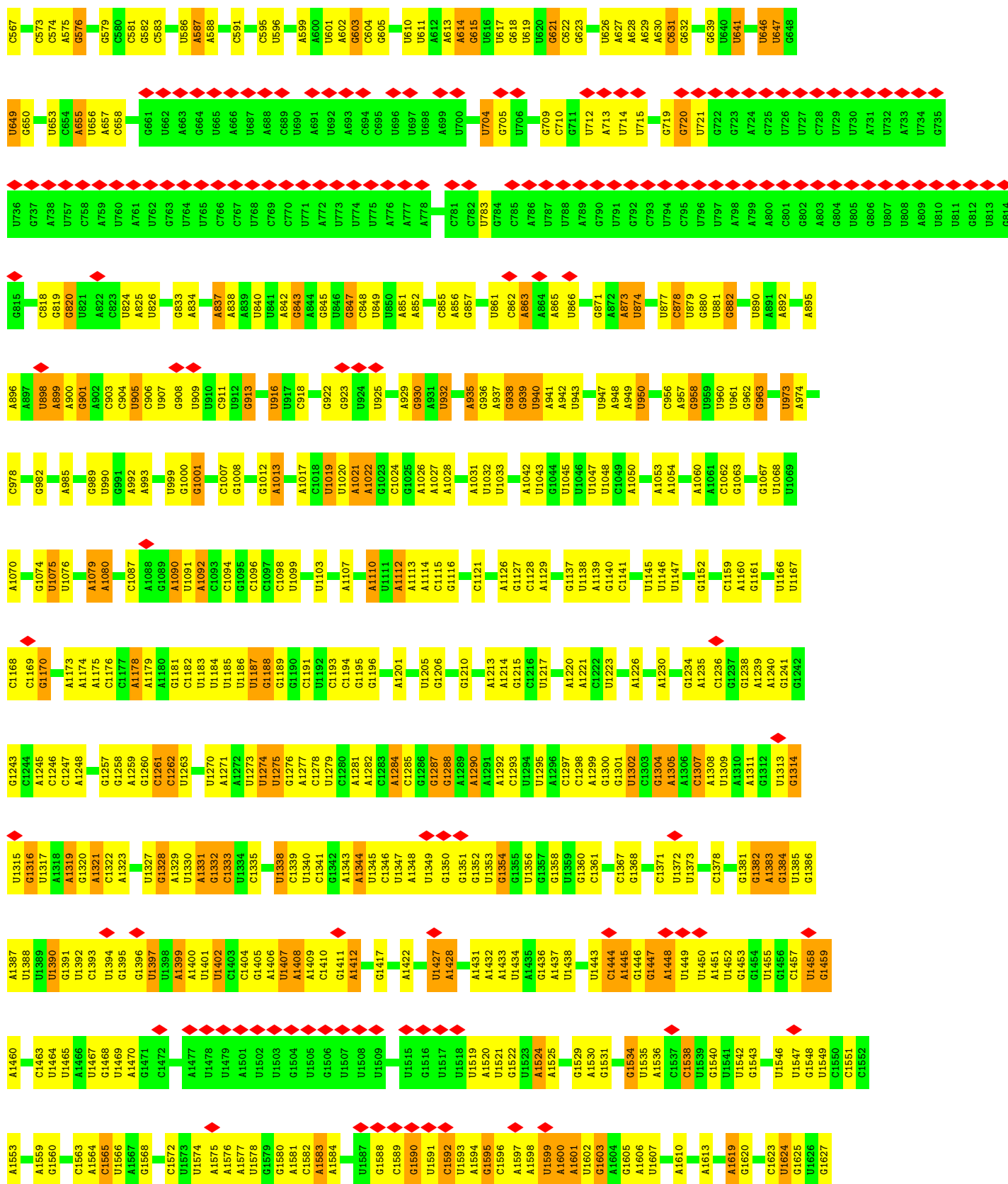


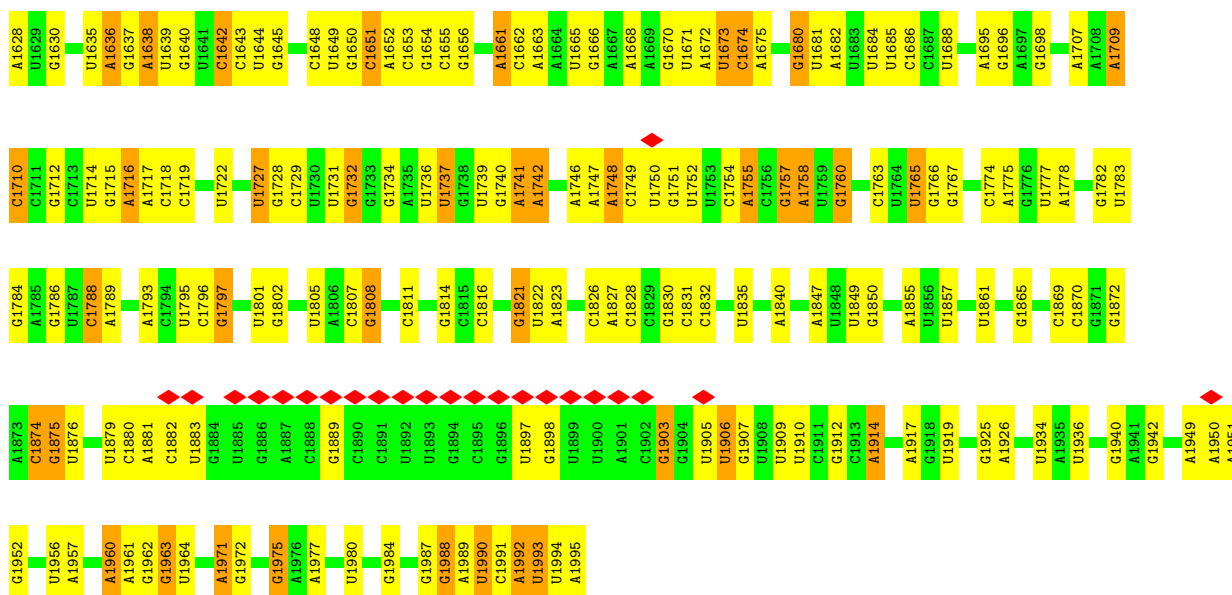
U3448	U3358	A3272	G3176	A3089	U2983	A2880	G2820	G2713	A2622	A2528	A2406	A2229	A2132
U3455	U3359	A3278	G3183	U3090	U2984	U2881	A2821	U2714	G2625	G2529	A2452	G2230	A2133
U3456	G3360	A3279	G3185	A3091	U2985	A2882	A2822	U2725	G2626	G2534	U2453	C2239	C2135
C3457	U3361	G3281	C3185	A3092	A2987	C2884	U2924	U2726	G2627	U2536	U2454	U2240	U2136
U3463	G3362	C3282	C3185	C3093	U2988	A2885	A2825	U2727	A2633	A2537	A2455	U2241	U2137
G3464	G3363	U3283	A3188	U3094	G2989	A2886	A2826	C2732	A2634	U2538	C2459	C2242	C2140
G3465	G3365	C3284	A3189	C3095	A2990	U2887	G2827	G2733	A2635	A2545	U2462	U2247	G2145
A3466	G3286	G3286	G3191	C3096	A2992	A2888	A2828	A2734	A2640	G2547	U2463	U2258	G2146
A3467	C3287	C3287	A3194	A3097	G2993	A2889	A2829	A2736	C2641	G2548	U2464	C2259	C2147
G3468	A3194	C3287	G3195	A3098	C2994	U2890	G2830	A2741	U2642	G2549	U2465	A2262	G2148
G3469	G3195	U2995	U2996	U3099	U2996	U2892	U2831	G2742	C2643	U2554	C2466	U2266	U2150
G3470	G3293	C2997	C2997	U3103	C2997	U2893	G2832	C2743	U2646	U2555	A2467	U2267	U2151
A3471	A3294	U2998	U2998	C3104	U2998	A2894	A2833	A2745	U2647	A2556	A2468	U2268	A2155
C3472	U3298	G2999	G3000	A3105	U2999	U2895	A2834	A2745	A2648	C2557	U2469	G2269	U2156
C3473	U3299	G3000	G3000	G3106	G3000	U2896	A2835	A2745	A2649	U2562	U2470	C2270	U2157
A3477	U3300	G3107	G3107	C3107	G3107	G2897	A2836	A2750	A2650	G2563	A2471	U2271	C2159
G3478	G3380	U3108	U3108	U3108	C3003	U2898	A2837	A2751	G2650	G2564	A2472	U2272	U2166
G3482	C3381	A3116	A3117	U3118	A3004	U2899	A2838	C2752	G2651	G2565	A2473	U2273	G2167
U3486	U3382	U3119	U3119	U3119	A3005	U2900	G2841	G2754	U2652	A2566	A2474	A2274	A2171
A3487	G3385	G3123	G3123	G3123	A3006	C2902	U2842	G2760	G2654	U2567	U2475	G2274	G2168
G3488	A3308	A3124	A3124	A3124	U3008	U2903	G2843	U2766	A2657	C2570	C2477	U2275	U2169
C3490	U3391	G3125	G3125	G3125	G3014	U2907	G2844	U2767	A2658	U2571	A2478	C2276	C2170
C3491	A3309	A3125	A3125	A3125	A3015	U2908	G2845	A2768	A2659	G2572	A2479	G2277	U2171
G3492	G3312	G3126	G3126	G3126	G3016	A2909	A2846	G2769	U2660	C2573	U2480	G2278	A2174
U3496	A3313	A3127	A3127	A3127	U3017	U2915	G2847	C2770	C2663	C2574	U2481	C2279	G2177
G3499	G3319	U3128	U3128	U3128	U3018	A2916	A2848	G2771	G2666	G2575	C2482	C2280	U2183
A3502	U3320	G3130	G3130	G3130	U3019	A2917	U2849	G2772	U2669	U2578	C2487	U2282	A2190
G3503	A3321	A3131	A3131	A3131	G3020	A2918	A2850	A2775	A2669	G2579	G2490	G2283	G2194
G3504	G3322	G3132	G3132	G3132	U3021	G2922	U2851	A2779	U2676	U2583	C2491	A2284	U2196
U3509	A3323	A3133	A3133	A3133	U3022	A2923	U2852	G2781	U2677	A2584	A2492	U2285	A2195
U3510	G3324	G3134	G3134	G3134	A3023	A2924	A2853	U2789	U2679	A2585	C2493	U2286	U2196
U3511	A3325	A3135	A3135	A3135	U3024	C2925	G2854	G2792	A2681	U2586	U2499	G2287	U2200
U3512	G3326	G3136	G3136	G3136	U3025	G2926	A2855	C2793	C2682	U2587	G2501	C2288	U2201
A3513	U3327	A3137	A3137	A3137	A3026	G2928	C2856	U2799	G2683	G2588	A2505	G2289	A2202
C3514	G3328	G3138	G3138	G3138	U3027	U2931	U2857	C2799	C2684	A2591	A2506	A2290	G2205
C3515	A3329	A3139	A3139	A3139	A3028	C2932	U2858	G2796	G2685	A2592	U2506	A2291	U2206
C3516	U3330	G3140	G3140	G3140	U3029	A2934	C2859	A2797	C2686	U2593	A2510	A2292	A2212
U3517	A3331	A3141	A3141	A3141	C3030	U2935	G2860	A2803	A2687	G2599	A2511	C2293	G2215
A3518	G3332	G3142	G3142	G3142	U3031	U2936	U2861	G2811	A2691	A2601	U2516	U2390	A2216
G3519	U3333	A3143	A3143	A3143	C3032	C2937	U2862	U2812	U2692	U2603	A2517	G2392	U2219
U3520	C3334	G3144	G3144	G3144	A3033	C2938	U2863	G2813	G2693	G2608	A2518	C2220	C2220
A3521	A3335	A3145	A3145	A3145	U3034	U2939	U2864	U2814	G2701	U2609	U2519	A2393	A2394
C3522	U3336	G3146	G3146	G3146	A3035	A2940	G2865	A2815	C2708	A2610	U2520	G2395	G2221
U3523	G3337	A3147	A3147	A3147	C3036	G2941	G2866	G2817	U2712	C2620	A2522	C2396	G2222
G3524	A3338	G3148	G3148	G3148	U3037	A2976	U2867	G2818	A2523	A2524	U2397	U2397	A2224
A3525	C3339	A3149	A3149	A3149	A3038	U2977	A2868	A2819	A2525	A2525	U2398	C2399	U2400
C3526	U3340	G3150	G3150	G3150	U3039	U2978	U2869	U2870	A2526	A2526	U2401	U2401	U2401
A3527	A3341	A3151	A3151	A3151	U3085	G2979	G2871	G2871	A2527	A2527	G2402	G2402	G2402
A3528	G3342	G3152	G3152	G3152	G3086	U2982	U2872	A2875	A2528	A2528	U2404	U2404	A2405
	A3343	A3174	A3174	A3174	U3087		A2875	U2876					



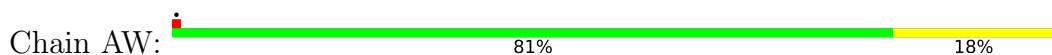
• Molecule 70: 18S ribosomal RNA



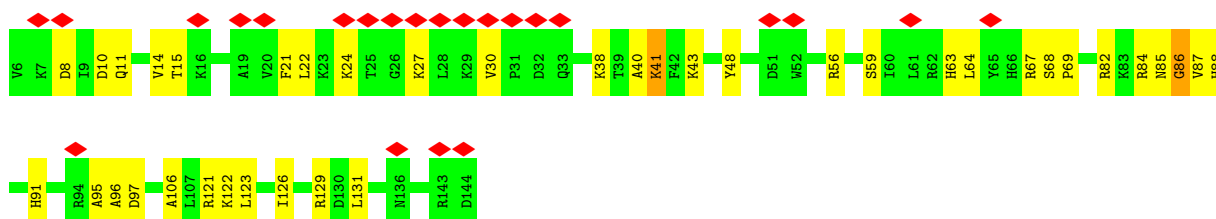




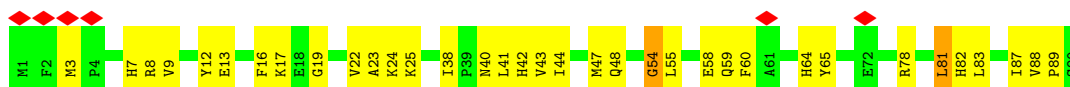
• Molecule 71: 40S ribosomal protein S15Aa



• Molecule 72: 40S ribosomal protein S19a

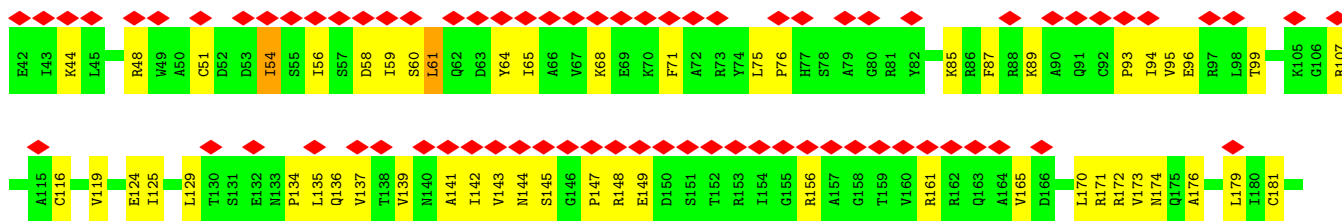


• Molecule 73: 40S ribosomal protein S10b

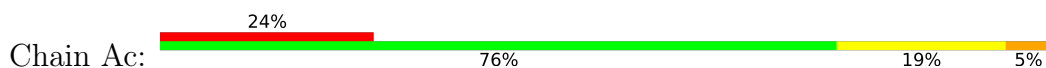


• Molecule 74: 40S ribosomal protein S5b

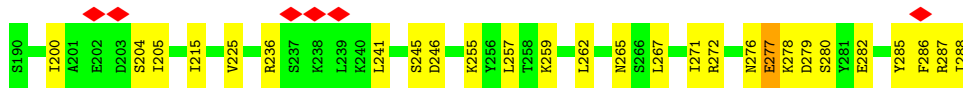
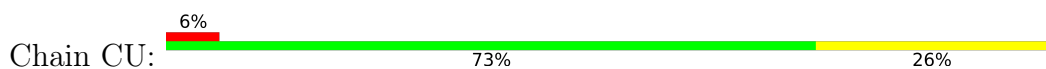




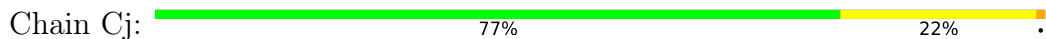
- Molecule 75: 40S ribosomal protein S28



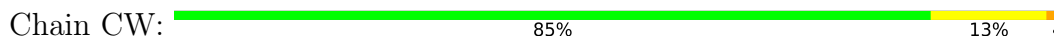
- Molecule 76: 60S ribosomal protein L22



- Molecule 77: Probable 60S ribosomal protein L37-A



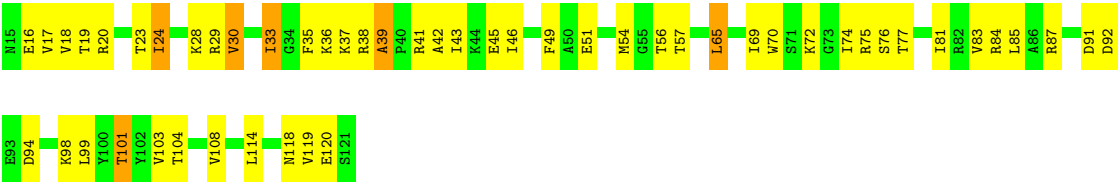
- Molecule 78: 60S ribosomal protein L24



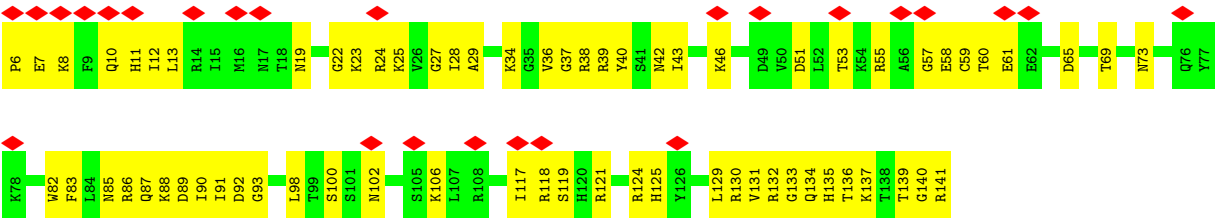
- Molecule 79: 60S ribosomal protein L34



- Molecule 80: 60S ribosomal protein L31



• Molecule 81: 40S ribosomal protein S18



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	185913	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.861	Depositor
Minimum map value	-0.593	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.035	Depositor
Map size ($\text{\AA}$)	426.00003, 426.00003, 426.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.065, 1.065, 1.065	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	CO	0.84	0/1700	0.97	5/2277 (0.2%)
2	CL	0.75	0/1726	1.23	26/2308 (1.1%)
3	CV	0.74	0/1014	0.79	2/1362 (0.1%)
4	CM	0.67	0/1326	0.88	2/1780 (0.1%)
5	Ca	0.99	0/1235	1.10	6/1640 (0.4%)
6	CN	0.97	0/1750	1.12	8/2335 (0.3%)
7	CI	0.50	1/1827 (0.1%)	0.78	3/2447 (0.1%)
8	CD	0.53	0/2379	0.75	2/3196 (0.1%)
9	CQ	0.92	0/1544	1.02	4/2069 (0.2%)
10	CR	0.60	0/1703	0.72	0/2255
11	CA	0.81	0/1970	0.91	4/2635 (0.2%)
12	CS	0.79	0/1491	1.18	10/1998 (0.5%)
13	CT	0.74	0/1326	1.01	4/1773 (0.2%)
14	CP	0.84	0/1529	0.92	0/2042
15	CX	0.67	0/1001	0.98	3/1348 (0.2%)
16	CY	0.76	0/1094	0.86	0/1456
17	CZ	0.47	0/1141	0.74	0/1517
18	Cr	0.88	0/1069	1.32	13/1432 (0.9%)
19	Ch	0.65	0/1024	0.86	0/1353
20	Cb	0.67	0/628	1.05	1/832 (0.1%)
21	CB	0.78	0/3356	1.01	9/4494 (0.2%)
22	CF	0.86	0/1931	0.92	3/2587 (0.1%)
23	Cc	0.52	0/779	0.64	0/1048
24	Ce	0.99	0/1132	1.07	5/1508 (0.3%)
25	Cf	0.86	0/1270	1.24	12/1696 (0.7%)
26	Ci	0.59	0/944	1.07	8/1250 (0.6%)
27	Ck	0.54	0/583	0.79	0/774
28	Cl	0.91	0/445	0.89	0/589
29	CC	0.89	1/3163 (0.0%)	1.11	12/4253 (0.3%)
30	Cm	0.55	0/435	0.89	2/575 (0.3%)
31	Cn	0.60	0/237	0.72	0/300
32	Cp	0.78	0/719	0.93	2/954 (0.2%)
33	Co	0.71	0/887	0.97	2/1162 (0.2%)
34	CJ	0.37	0/1494	0.88	7/2001 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	CH	0.57	0/1519	0.83	4/2042 (0.2%)
36	CE	0.63	0/1883	1.13	10/2514 (0.4%)
37	CG	0.55	1/1968 (0.1%)	0.86	2/2637 (0.1%)
38	A9	0.73	0/714	0.70	0/1112
39	A7	0.72	0/2854	0.61	0/4447
40	A8	0.93	0/2932	0.72	0/4568
41	Ag	0.28	0/2574	0.71	1/3506 (0.0%)
42	AU	0.30	0/825	0.71	0/1111
43	AO	0.32	0/965	0.80	2/1295 (0.2%)
44	AX	0.34	0/1152	0.79	1/1540 (0.1%)
45	AM	0.32	0/937	0.93	2/1260 (0.2%)
46	Ad	0.28	0/443	0.75	0/589
47	AN	0.35	0/1225	0.68	3/1641 (0.2%)
48	AL	0.39	0/1296	0.73	2/1725 (0.1%)
49	AR	0.31	0/993	0.83	2/1333 (0.2%)
50	AP	0.29	0/1036	0.82	0/1383
51	AB	0.29	0/1825	0.74	3/2448 (0.1%)
52	AA	0.28	0/1777	0.70	0/2422
53	AV	0.28	0/622	0.67	0/835
54	AY	0.26	0/1032	0.78	4/1373 (0.3%)
55	AZ	0.31	0/616	0.83	0/826
56	Aa	0.38	0/883	0.78	2/1184 (0.2%)
57	Ab	0.25	0/668	0.67	0/898
58	AD	0.26	0/1808	0.77	3/2427 (0.1%)
59	Ae	0.27	0/475	0.80	2/625 (0.3%)
60	Af	0.29	0/672	0.86	4/887 (0.5%)
61	AJ	0.28	0/1526	0.72	2/2037 (0.1%)
62	AE	0.29	0/2096	0.66	0/2819
63	AC	0.32	0/1785	0.74	5/2415 (0.2%)
64	AG	0.28	0/1891	0.70	0/2519
65	AH	0.28	0/1593	0.74	0/2145
66	AI	0.41	0/1689	0.94	5/2250 (0.2%)
67	AQ	0.30	0/1202	0.92	6/1608 (0.4%)
68	Cz	0.31	0/1727	0.80	0/2308
69	A5	0.87	3/86147 (0.0%)	0.75	56/134004 (0.0%)
70	B2	0.34	0/43887	0.44	2/68161 (0.0%)
71	AW	0.33	0/1046	0.58	0/1402
72	AT	0.26	0/1019	0.75	0/1367
73	AK	0.33	0/786	0.90	2/1064 (0.2%)
74	AF	0.29	0/1501	0.73	2/2017 (0.1%)
75	Ac	0.31	0/502	0.82	2/670 (0.3%)
76	CU	0.41	0/838	0.88	4/1123 (0.4%)
77	Cj	1.03	0/717	0.95	0/950

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	CW	0.63	0/515	0.87	2/683 (0.3%)
79	Cg	0.78	0/855	0.89	1/1142 (0.1%)
80	Cd	0.20	0/908	0.46	0/1221
81	AS	0.23	0/1135	0.74	2/1521 (0.1%)
All	All	0.68	6/232911 (0.0%)	0.76	293/341300 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	CO	0	9
2	CL	0	14
4	CM	0	2
5	Ca	0	5
6	CN	0	7
7	CI	0	5
8	CD	0	5
9	CQ	0	5
10	CR	0	3
11	CA	0	4
12	CS	0	11
13	CT	0	8
14	CP	0	3
16	CY	0	2
18	Cr	0	15
19	Ch	0	5
20	Cb	0	4
21	CB	0	18
22	CF	0	4
24	Ce	0	3
25	Cf	0	11
26	Ci	0	7
27	Ck	0	2
29	CC	0	15
30	Cm	0	2
33	Co	0	3
34	CJ	0	4
35	CH	0	4
36	CE	0	25
37	CG	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
43	AO	0	4
44	AX	0	1
45	AM	0	3
46	Ad	0	1
50	AP	0	3
51	AB	0	4
52	AA	0	2
53	AV	0	2
54	AY	0	1
55	AZ	0	4
56	Aa	0	2
57	Ab	0	1
58	AD	0	6
59	Ae	0	1
60	Af	0	10
61	AJ	0	4
62	AE	0	1
63	AC	0	2
64	AG	0	2
65	AH	0	3
66	AI	0	2
67	AQ	0	5
68	Cz	0	2
72	AT	0	3
74	AF	0	2
75	Ac	0	1
76	CU	0	1
78	CW	0	1
79	Cg	0	1
80	Cd	0	1
All	All	0	290

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	CI	132	GLY	C-N	-9.40	1.18	1.33
37	CG	133	GLU	C-N	6.15	1.38	1.33
29	CC	79	ILE	CG1-CD1	-5.77	1.29	1.51
69	A5	1795	A	C5-C6	-5.76	1.29	1.41
69	A5	1383	A	O3'-P	5.18	1.69	1.61
69	A5	1383	A	O5'-C5'	5.01	1.50	1.42

All (293) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	CI	132	GLY	CA-C-N	11.48	137.56	121.61
7	CI	132	GLY	C-N-CA	11.48	137.56	121.61
29	CC	195	GLY	CA-C-N	10.72	140.99	121.70
29	CC	195	GLY	C-N-CA	10.72	140.99	121.70
25	Cf	46	ARG	N-CA-C	10.55	124.89	108.12
21	CB	324	GLY	N-CA-C	10.53	138.14	113.18
69	A5	3677	U	N1-C1'-C2'	10.32	127.48	112.00
29	CC	364	GLU	CA-C-N	10.04	139.78	121.70
29	CC	364	GLU	C-N-CA	10.04	139.78	121.70
12	CS	89	GLY	N-CA-C	9.32	135.27	113.18
69	A5	1383	A	C4'-C3'-O3'	8.97	126.46	113.00
1	CO	202	GLY	N-CA-C	8.94	130.63	114.46
2	CL	159	GLU	CA-C-N	8.91	143.53	121.80
2	CL	159	GLU	C-N-CA	8.91	143.53	121.80
25	Cf	48	GLY	N-CA-C	8.72	133.84	113.18
26	Ci	4	ARG	CA-C-N	8.40	136.82	121.70
26	Ci	4	ARG	C-N-CA	8.40	136.82	121.70
18	Cr	39	VAL	N-CA-C	8.39	121.68	113.71
21	CB	323	TYR	CA-CB-CG	8.13	128.53	113.90
15	CX	186	VAL	CA-C-N	8.12	146.50	127.00
15	CX	186	VAL	C-N-CA	8.12	146.50	127.00
13	CT	144	LEU	CA-C-N	7.82	135.77	121.70
13	CT	144	LEU	C-N-CA	7.82	135.77	121.70
69	A5	1801	U	O4'-C1'-N1	7.77	120.16	108.50
29	CC	297	LYS	CA-C-N	7.74	135.63	121.70
29	CC	297	LYS	C-N-CA	7.74	135.63	121.70
2	CL	160	GLN	N-CA-C	7.74	126.91	109.81
69	A5	1699	A	N1-C6-N6	-7.48	96.15	118.60
61	AJ	5	ARG	CA-C-N	7.48	135.16	121.70
61	AJ	5	ARG	C-N-CA	7.48	135.16	121.70
73	AK	54	GLY	CA-C-N	7.46	135.13	121.70
73	AK	54	GLY	C-N-CA	7.46	135.13	121.70
67	AQ	144	GLN	CA-C-N	7.45	135.77	121.54
67	AQ	144	GLN	C-N-CA	7.45	135.77	121.54
45	AM	39	VAL	CA-C-N	7.42	135.05	121.70
45	AM	39	VAL	C-N-CA	7.42	135.05	121.70
76	CU	278	LYS	CA-C-N	7.37	135.62	121.54
76	CU	278	LYS	C-N-CA	7.37	135.62	121.54
15	CX	186	VAL	C-N-CD	-7.33	104.47	120.60
33	Co	47	GLY	CA-C-N	7.31	135.51	121.54
33	Co	47	GLY	C-N-CA	7.31	135.51	121.54
69	A5	839	A	P-O3'-C3'	7.21	131.02	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	CE	65	SER	CA-C-N	7.06	134.41	121.70
36	CE	65	SER	C-N-CA	7.06	134.41	121.70
69	A5	3677	U	O4'-C1'-N1	6.98	118.97	108.50
69	A5	1799	U	C6-N1-C1'	-6.95	100.35	121.20
12	CS	173	ARG	CA-C-N	6.95	134.81	121.54
12	CS	173	ARG	C-N-CA	6.95	134.81	121.54
24	Ce	128	LEU	CA-C-N	6.92	134.15	121.70
24	Ce	128	LEU	C-N-CA	6.92	134.15	121.70
69	A5	840	U	O5'-P-OP1	-6.89	87.32	108.00
69	A5	1801	U	C2'-C3'-O3'	6.89	124.03	113.70
25	Cf	110	ARG	CA-C-N	6.87	136.04	122.31
25	Cf	110	ARG	C-N-CA	6.87	136.04	122.31
8	CD	188	LYS	CA-C-N	6.85	134.04	121.70
8	CD	188	LYS	C-N-CA	6.85	134.04	121.70
69	A5	1801	U	C5'-C4'-O4'	6.85	120.07	109.80
18	Cr	76	ARG	CA-C-N	6.81	143.34	127.00
18	Cr	76	ARG	C-N-CA	6.81	143.34	127.00
4	CM	153	ALA	CA-C-N	6.79	133.93	121.70
4	CM	153	ALA	C-N-CA	6.79	133.93	121.70
60	Af	151	SER	CA-C-N	6.75	133.85	121.70
60	Af	151	SER	C-N-CA	6.75	133.85	121.70
2	CL	157	LYS	CA-C-N	6.75	133.84	121.70
2	CL	157	LYS	C-N-CA	6.75	133.84	121.70
66	AI	133	GLU	CA-C-N	6.73	133.82	121.70
66	AI	133	GLU	C-N-CA	6.73	133.82	121.70
2	CL	163	VAL	CA-C-N	6.72	133.79	121.70
2	CL	163	VAL	C-N-CA	6.72	133.79	121.70
69	A5	1566	U	P-O3'-C3'	6.71	130.26	120.20
26	Ci	10	GLY	CA-C-N	6.69	132.09	122.40
26	Ci	10	GLY	C-N-CA	6.69	132.09	122.40
69	A5	1799	U	C2-N1-C1'	6.68	137.74	117.70
69	A5	3473	C	O5'-C5'-C4'	6.67	121.51	111.50
34	CJ	159	GLN	CA-C-N	6.67	133.70	121.70
34	CJ	159	GLN	C-N-CA	6.67	133.70	121.70
36	CE	193	VAL	CA-C-N	6.66	142.97	127.00
36	CE	193	VAL	C-N-CA	6.66	142.97	127.00
18	Cr	48	VAL	N-CA-CB	-6.56	102.10	112.07
2	CL	169	VAL	CA-C-N	6.49	133.39	121.70
2	CL	169	VAL	C-N-CA	6.49	133.39	121.70
69	A5	3841	C	N1-C1'-C2'	6.49	123.73	114.00
12	CS	137	THR	CA-C-N	-6.48	113.74	121.90
12	CS	137	THR	C-N-CA	-6.48	113.74	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	CB	40	PRO	N-CA-C	6.41	125.67	112.47
12	CS	63	SER	N-CA-C	6.37	120.07	110.64
13	CT	149	ALA	CA-C-N	6.36	133.15	121.70
13	CT	149	ALA	C-N-CA	6.36	133.15	121.70
43	AO	99	ALA	CA-C-N	6.35	133.12	121.70
43	AO	99	ALA	C-N-CA	6.35	133.12	121.70
47	AN	134	VAL	N-CA-C	-6.34	106.00	113.42
6	CN	106	VAL	N-CA-C	-6.33	106.62	112.96
69	A5	3140	G	OP1-P-O3'	6.33	126.98	108.00
81	AS	89	ASP	CA-C-N	6.32	133.08	121.70
81	AS	89	ASP	C-N-CA	6.32	133.08	121.70
1	CO	133	SER	CA-C-N	6.29	133.56	121.54
1	CO	133	SER	C-N-CA	6.29	133.56	121.54
69	A5	2750	A	P-O3'-C3'	6.27	129.60	120.20
18	Cr	87	LYS	N-CA-C	6.25	124.12	110.80
5	Ca	47	ASP	CA-C-N	6.25	132.94	121.70
5	Ca	47	ASP	C-N-CA	6.25	132.94	121.70
5	Ca	93	LYS	CA-C-N	6.23	132.91	121.70
5	Ca	93	LYS	C-N-CA	6.23	132.91	121.70
9	CQ	156	PRO	N-CA-C	6.22	125.28	112.47
69	A5	1784	A	P-O3'-C3'	6.22	129.53	120.20
69	A5	1801	U	O4'-C4'-C3'	-6.20	97.80	104.00
69	A5	3845	A	C4'-C3'-O3'	6.16	122.24	113.00
69	A5	1801	U	C4'-C3'-O3'	6.15	122.22	113.00
47	AN	58	HIS	CA-C-N	6.14	132.75	121.70
47	AN	58	HIS	C-N-CA	6.14	132.75	121.70
69	A5	3473	C	C4'-C3'-O3'	6.12	122.18	113.00
18	Cr	47	ILE	CA-C-N	6.11	130.57	121.77
18	Cr	47	ILE	C-N-CA	6.11	130.57	121.77
29	CC	93	GLY	N-CA-C	6.11	127.66	113.18
24	Ce	52	TYR	CA-CB-CG	-6.09	102.93	113.90
63	AC	39	ASP	CA-C-N	6.08	132.64	121.70
63	AC	39	ASP	C-N-CA	6.08	132.64	121.70
21	CB	270	GLY	CA-C-N	6.06	133.11	121.54
21	CB	270	GLY	C-N-CA	6.06	133.11	121.54
69	A5	2750	A	C2'-C3'-O3'	6.04	118.56	109.50
2	CL	135	ALA	CA-C-N	6.04	132.57	121.70
2	CL	135	ALA	C-N-CA	6.04	132.57	121.70
18	Cr	76	ARG	C-N-CD	-6.04	107.32	120.60
11	CA	1	MET	CB-CG-SD	6.04	130.80	112.70
9	CQ	116	ALA	CA-C-N	6.03	132.56	121.70
9	CQ	116	ALA	C-N-CA	6.03	132.56	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	CI	216	VAL	N-CA-C	-6.03	106.93	112.96
34	CJ	102	GLU	CA-C-N	6.03	132.55	121.70
34	CJ	102	GLU	C-N-CA	6.03	132.55	121.70
67	AQ	117	TYR	CA-C-N	5.98	132.96	121.54
67	AQ	117	TYR	C-N-CA	5.98	132.96	121.54
35	CH	109	VAL	CA-C-N	5.94	132.66	121.97
35	CH	109	VAL	C-N-CA	5.94	132.66	121.97
69	A5	1688	A	P-O3'-C3'	5.93	129.09	120.20
69	A5	3841	C	O4'-C1'-N1	5.92	117.09	108.20
22	CF	219	THR	N-CA-C	-5.92	96.73	109.81
56	Aa	107	ALA	CA-C-N	5.92	132.35	121.70
56	Aa	107	ALA	C-N-CA	5.92	132.35	121.70
67	AQ	3	GLN	CA-C-N	5.91	132.34	121.70
67	AQ	3	GLN	C-N-CA	5.91	132.34	121.70
69	A5	3594	A	O5'-P-OP1	-5.89	90.34	108.00
2	CL	4	GLY	N-CA-C	5.88	127.13	113.18
2	CL	147	THR	CA-C-N	5.88	132.77	121.54
2	CL	147	THR	C-N-CA	5.88	132.77	121.54
1	CO	33	GLY	N-CA-C	5.86	127.06	113.18
49	AR	94	ASP	CA-C-N	5.85	132.24	121.70
49	AR	94	ASP	C-N-CA	5.85	132.24	121.70
69	A5	2093	U	P-O3'-C3'	5.85	128.97	120.20
69	A5	3754	C	O5'-P-OP1	5.83	125.50	108.00
69	A5	1382	U	O3'-P-O5'	5.82	112.72	104.00
69	A5	3472	A	P-O3'-C3'	5.81	128.92	120.20
2	CL	158	ASN	CA-C-N	5.80	132.14	121.70
2	CL	158	ASN	C-N-CA	5.80	132.14	121.70
69	A5	1383	A	OP1-P-O3'	5.78	125.35	108.00
74	AF	217	LYS	CA-C-N	5.78	135.10	124.82
74	AF	217	LYS	C-N-CA	5.78	135.10	124.82
36	CE	193	VAL	C-N-CD	-5.76	107.93	120.60
69	A5	296	C	C2'-C3'-O3'	5.75	122.32	113.70
20	Cb	7	HIS	N-CA-C	5.73	123.01	110.80
48	AL	52	TYR	CA-C-N	-5.71	117.37	122.97
48	AL	52	TYR	C-N-CA	-5.71	117.37	122.97
37	CG	43	ASN	N-CA-C	5.68	122.91	110.80
66	AI	140	THR	CA-C-N	5.68	132.39	121.54
66	AI	140	THR	C-N-CA	5.68	132.39	121.54
54	AY	103	GLN	CA-C-N	5.66	131.89	121.70
54	AY	103	GLN	C-N-CA	5.66	131.89	121.70
58	AD	182	GLY	CA-C-N	5.64	127.61	121.97
58	AD	182	GLY	C-N-CA	5.64	127.61	121.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	Cg	34	TYR	CB-CA-C	5.64	119.06	109.80
12	CS	176	PHE	N-CA-C	5.64	117.57	110.24
18	Cr	80	ASN	N-CA-C	5.63	122.79	110.80
24	Ce	15	ARG	N-CA-C	5.62	122.78	110.80
34	CJ	96	GLU	CA-CB-CG	5.62	125.35	114.10
25	Cf	46	ARG	N-CA-CB	-5.59	101.65	111.04
21	CB	271	GLN	N-CA-C	5.57	122.67	110.80
66	AI	148	MET	CA-C-O	-5.57	112.74	119.59
24	Ce	7	TYR	CA-CB-CG	5.55	123.89	113.90
69	A5	3677	U	C2'-C3'-O3'	-5.55	105.37	113.70
6	CN	79	CYS	CA-C-N	5.54	132.11	121.54
6	CN	79	CYS	C-N-CA	5.54	132.11	121.54
11	CA	213	GLY	N-CA-C	5.52	126.27	113.18
54	AY	4	THR	CA-C-N	5.52	132.09	121.54
54	AY	4	THR	C-N-CA	5.52	132.09	121.54
69	A5	1193	A	P-O3'-C3'	5.52	128.49	120.20
51	AB	182	ALA	CA-C-N	5.52	132.09	121.54
51	AB	182	ALA	C-N-CA	5.52	132.09	121.54
34	CJ	160	HIS	N-CA-C	5.51	126.43	111.00
6	CN	76	PRO	CA-C-N	5.51	132.06	121.54
6	CN	76	PRO	C-N-CA	5.51	132.06	121.54
25	Cf	16	LYS	CA-C-N	5.50	131.60	121.70
25	Cf	16	LYS	C-N-CA	5.50	131.60	121.70
69	A5	1699	A	C5-C6-N6	5.49	140.17	123.70
34	CJ	103	ASN	N-CA-C	5.48	126.34	111.00
2	CL	19	ARG	CB-CG-CD	5.44	123.80	111.30
2	CL	66	HIS	CA-C-N	5.43	129.86	120.58
2	CL	66	HIS	C-N-CA	5.43	129.86	120.58
1	CO	113	PRO	N-CA-C	5.42	123.63	112.47
76	CU	236	ARG	CA-C-N	5.42	131.88	121.54
76	CU	236	ARG	C-N-CA	5.42	131.88	121.54
36	CE	168	PHE	CA-C-N	5.41	129.37	121.31
36	CE	168	PHE	C-N-CA	5.41	129.37	121.31
29	CC	392	VAL	N-CA-C	-5.41	107.71	112.90
69	A5	1115	A	C4'-C3'-O3'	5.40	121.10	113.00
69	A5	1689	G	O5'-P-OP2	5.40	124.19	108.00
9	CQ	65	ARG	CG-CD-NE	5.39	123.86	112.00
69	A5	1713	U	C5'-C4'-O4'	5.38	117.87	109.80
26	Ci	24	LYS	CA-C-N	5.38	129.74	121.19
26	Ci	24	LYS	C-N-CA	5.38	129.74	121.19
29	CC	204	ARG	CA-C-N	5.37	131.63	121.97
29	CC	204	ARG	C-N-CA	5.37	131.63	121.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
69	A5	424	G	O4'-C1'-N9	5.37	116.25	108.20
2	CL	162	ALA	CA-C-N	5.36	131.35	121.70
2	CL	162	ALA	C-N-CA	5.36	131.35	121.70
41	Ag	271	LEU	CA-CB-CG	5.36	135.06	116.30
25	Cf	50	LEU	N-CA-C	-5.36	102.08	110.17
69	A5	1688	A	O4'-C1'-N9	5.35	116.22	108.20
18	Cr	28	PRO	CA-C-O	-5.34	110.88	120.60
69	A5	839	A	C4-N9-C1'	-5.34	110.28	126.30
69	A5	1689	G	P-O3'-C3'	5.34	128.20	120.20
70	B2	25	U	P-O3'-C3'	5.32	128.18	120.20
69	A5	2037	C	O4'-C1'-N1	5.31	116.16	108.20
6	CN	188	ARG	N-CA-C	-5.29	99.53	110.80
78	CW	25	ASP	CA-C-N	5.29	131.23	121.70
78	CW	25	ASP	C-N-CA	5.29	131.23	121.70
69	A5	3846	U	C4'-C3'-O3'	5.29	120.94	113.00
2	CL	74	GLY	CA-C-N	5.29	131.64	121.54
2	CL	74	GLY	C-N-CA	5.29	131.64	121.54
63	AC	101	ALA	CA-C-N	5.29	131.22	121.70
63	AC	101	ALA	C-N-CA	5.29	131.22	121.70
25	Cf	46	ARG	CA-C-N	5.29	131.63	121.54
25	Cf	46	ARG	C-N-CA	5.29	131.63	121.54
32	Cp	59	ARG	CA-C-N	5.28	131.62	121.54
32	Cp	59	ARG	C-N-CA	5.28	131.62	121.54
26	Ci	4	ARG	N-CA-C	5.27	121.52	113.51
11	CA	1	MET	CA-C-N	5.27	134.35	122.29
11	CA	1	MET	C-N-CA	5.27	134.35	122.29
21	CB	299	ILE	CA-C-N	5.26	131.59	121.54
21	CB	299	ILE	C-N-CA	5.26	131.59	121.54
5	Ca	63	HIS	N-CA-C	5.25	117.06	110.91
5	Ca	116	GLY	N-CA-C	5.24	125.61	113.18
26	Ci	44	THR	N-CA-CB	5.24	119.35	110.49
25	Cf	108	PRO	CA-N-CD	-5.23	104.68	112.00
2	CL	97	VAL	N-CA-C	5.22	120.20	109.34
18	Cr	91	ARG	CA-C-N	5.22	131.51	121.54
18	Cr	91	ARG	C-N-CA	5.22	131.51	121.54
29	CC	269	THR	N-CA-C	-5.22	99.68	110.80
25	Cf	140	PRO	N-CA-C	5.21	123.21	112.47
69	A5	2194	G	OP2-P-O3'	5.21	123.62	108.00
22	CF	235	GLY	CA-C-N	5.20	131.48	121.54
22	CF	235	GLY	C-N-CA	5.20	131.48	121.54
37	CG	83	PRO	N-CA-C	5.20	117.04	110.70
69	A5	3839	A	P-O3'-C3'	5.19	127.99	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	CV	49	LEU	CA-C-N	5.19	131.45	121.54
3	CV	49	LEU	C-N-CA	5.19	131.45	121.54
44	AX	89	GLY	N-CA-C	-5.18	100.90	113.18
69	A5	1712	C	C4'-C3'-O3'	5.18	120.77	113.00
69	A5	3846	U	OP1-P-O3'	5.18	123.53	108.00
36	CE	29	GLY	N-CA-C	-5.17	100.92	113.18
69	A5	3627	C	C4'-C3'-O3'	5.17	117.15	109.40
75	Ac	38	ILE	CA-C-N	5.17	127.42	120.50
75	Ac	38	ILE	C-N-CA	5.17	127.42	120.50
63	AC	159	LYS	CA-CB-CG	5.16	124.42	114.10
18	Cr	39	VAL	CB-CA-C	-5.15	105.78	110.63
69	A5	1799	U	O4'-C1'-N1	5.15	116.23	108.50
6	CN	181	SER	CA-C-N	-5.14	114.36	122.08
6	CN	181	SER	C-N-CA	-5.14	114.36	122.08
69	A5	3627	C	C2'-C3'-O3'	5.14	117.21	109.50
69	A5	1095	G	N9-C1'-C2'	5.14	119.71	112.00
69	A5	1689	G	OP1-P-OP2	-5.13	104.22	119.60
29	CC	92	GLN	N-CA-C	5.12	121.70	110.80
12	CS	176	PHE	CA-C-N	5.09	130.87	121.70
12	CS	176	PHE	C-N-CA	5.09	130.87	121.70
36	CE	88	LYS	CA-C-N	5.09	131.27	121.54
36	CE	88	LYS	C-N-CA	5.09	131.27	121.54
69	A5	1383	A	C5'-C4'-C3'	5.09	123.64	116.00
2	CL	46	PHE	N-CA-C	-5.09	98.57	109.81
69	A5	296	C	P-O3'-C3'	5.08	127.83	120.20
30	Cm	113	LYS	CA-C-N	5.08	131.25	121.54
30	Cm	113	LYS	C-N-CA	5.08	131.25	121.54
35	CH	48	PRO	CA-C-N	5.08	130.53	122.61
35	CH	48	PRO	C-N-CA	5.08	130.53	122.61
58	AD	201	GLY	N-CA-C	5.07	122.68	112.34
69	A5	224	U	O3'-P-O5'	5.06	111.58	104.00
51	AB	120	TRP	CA-CB-CG	-5.04	104.03	113.60
70	B2	1765	U	P-O3'-C3'	5.03	127.75	120.20
2	CL	61	PRO	N-CA-C	5.03	122.84	112.47
60	Af	88	PRO	CA-C-N	5.02	131.13	121.54
60	Af	88	PRO	C-N-CA	5.02	131.13	121.54
69	A5	839	A	C4'-C3'-O3'	5.02	116.93	109.40
12	CS	151	LYS	N-CA-C	5.01	118.64	111.02
21	CB	83	PRO	N-CA-C	5.01	118.95	111.14
59	Ae	95	GLU	CA-C-N	5.00	131.09	121.54
59	Ae	95	GLU	C-N-CA	5.00	131.09	121.54

There are no chirality outliers.

All (290) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
52	AA	200	ASP	Peptide
52	AA	7	ILE	Peptide
51	AB	118	LYS	Peptide
51	AB	119	LYS	Peptide
51	AB	183	ASP	Peptide
51	AB	215	ILE	Peptide
63	AC	186	GLY	Peptide
63	AC	241	GLU	Peptide
58	AD	145	ARG	Peptide
58	AD	195	ASP	Peptide
58	AD	199	LYS	Peptide
58	AD	204	LYS	Peptide
58	AD	205	PRO	Peptide
58	AD	224	PRO	Peptide
62	AE	240	LYS	Peptide
74	AF	218	LYS	Peptide
74	AF	61	LEU	Peptide
64	AG	218	LYS	Peptide
64	AG	99	GLY	Peptide
65	AH	113	LYS	Peptide
65	AH	187	PHE	Peptide
65	AH	64	ILE	Peptide
66	AI	49	ARG	Peptide
66	AI	98	LYS	Peptide
61	AJ	139	ARG	Peptide
61	AJ	170	ARG	Peptide
61	AJ	5	ARG	Peptide
61	AJ	9	VAL	Peptide
45	AM	101	ILE	Peptide
45	AM	22	ASN	Peptide
45	AM	60	ALA	Peptide
43	AO	127	GLY	Peptide
43	AO	137	SER	Peptide
43	AO	98	ARG	Peptide
43	AO	99	ALA	Peptide
50	AP	31	MET	Peptide
50	AP	53	LYS	Peptide
50	AP	88	ILE	Peptide
67	AQ	114	LEU	Peptide
67	AQ	17	ARG	Peptide
67	AQ	19	LYS	Peptide
67	AQ	3	GLN	Peptide

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Mol	Chain	Res	Type	Group
67	AQ	45	GLU	Peptide
72	AT	10	ASP	Peptide
72	AT	41	LYS	Peptide
72	AT	95	ALA	Peptide
53	AV	10	ASP	Peptide
53	AV	40	ASP	Peptide
44	AX	89	GLY	Peptide
54	AY	86	PHE	Peptide
55	AZ	57	LEU	Peptide
55	AZ	58	TYR	Peptide
55	AZ	59	LYS	Peptide
55	AZ	60	GLU	Peptide
56	Aa	85	ARG	Peptide
56	Aa	99	LEU	Peptide
57	Ab	49	HIS	Peptide
75	Ac	20	GLN	Peptide
46	Ad	33	LYS	Peptide
59	Ae	96	LYS	Peptide
60	Af	110	GLU	Peptide
60	Af	111	ASN	Peptide
60	Af	135	HIS	Peptide
60	Af	136	GLU	Peptide
60	Af	143	LYS	Peptide
60	Af	144	CYS	Peptide
60	Af	151	SER	Peptide
60	Af	152	LYS	Peptide
60	Af	87	THR	Peptide
60	Af	89	LYS	Peptide
11	CA	13	GLY	Peptide
11	CA	142	ASP	Peptide
11	CA	195	SER	Peptide
11	CA	196	TRP	Peptide
21	CB	145	SER	Peptide
21	CB	17	TYR	Peptide
21	CB	18	PRO	Peptide
21	CB	270	GLY	Peptide
21	CB	290	GLY	Peptide
21	CB	292	HIS	Peptide
21	CB	3	HIS	Peptide
21	CB	311	ASP	Peptide
21	CB	323	TYR	Peptide
21	CB	325	GLU	Peptide

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Mol	Chain	Res	Type	Group
21	CB	33	PRO	Peptide
21	CB	334	LYS	Peptide
21	CB	35	ASP	Peptide
21	CB	39	LYS	Peptide
21	CB	393	LYS	Peptide
21	CB	40	PRO	Peptide
21	CB	56	ILE	Peptide
21	CB	63	PRO	Peptide
29	CC	105	PHE	Peptide
29	CC	134	SER	Peptide
29	CC	17	ASN	Peptide
29	CC	203	ARG	Peptide
29	CC	297	LYS	Peptide
29	CC	309	ARG	Peptide
29	CC	312	VAL	Peptide
29	CC	314	ARG	Peptide
29	CC	316	VAL	Peptide
29	CC	6	ALA	Peptide
29	CC	69	SER	Peptide
29	CC	8	PRO	Peptide
29	CC	91	GLY	Peptide,Mainchain
29	CC	92	GLN	Peptide
8	CD	175	HIS	Peptide
8	CD	187	THR	Peptide
8	CD	43	LYS	Peptide
8	CD	8	LYS	Peptide
8	CD	9	ASN	Peptide
36	CE	170	ARG	Peptide
36	CE	175	LYS	Peptide
36	CE	19	LYS	Peptide
36	CE	191	ARG	Peptide
36	CE	193	VAL	Peptide
36	CE	221	PHE	Peptide
36	CE	228	ASN	Peptide
36	CE	23	ASN	Peptide
36	CE	237	TYR	Peptide
36	CE	239	HIS	Peptide
36	CE	25	TYR	Peptide
36	CE	26	LEU	Peptide
36	CE	32	ARG	Peptide
36	CE	35	LYS	Peptide
36	CE	48	LYS	Peptide

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Mol	Chain	Res	Type	Group
36	CE	60	VAL	Peptide
36	CE	64	LYS	Peptide
36	CE	68	SER	Peptide
36	CE	69	TYR	Peptide
36	CE	71	THR	Peptide
36	CE	72	LYS	Peptide
36	CE	75	VAL	Peptide
36	CE	82	ALA	Peptide
36	CE	83	ASN	Peptide
36	CE	88	LYS	Peptide
22	CF	171	PRO	Peptide
22	CF	235	GLY	Peptide,Mainchain
22	CF	99	ARG	Peptide
37	CG	168	PRO	Peptide
37	CG	213	ASP	Peptide
37	CG	41	PRO	Peptide
37	CG	42	LYS	Peptide
37	CG	48	GLN	Peptide
37	CG	82	PRO	Peptide
37	CG	87	GLN	Peptide
37	CG	88	PHE	Peptide
37	CG	93	ASP	Peptide
35	CH	106	ASN	Peptide
35	CH	162	SER	Peptide
35	CH	22	ALA	Peptide
35	CH	40	HIS	Peptide
7	CI	118	ALA	Peptide
7	CI	13	LYS	Peptide
7	CI	188	ASN	Peptide
7	CI	199	TYR	Peptide
7	CI	9	TYR	Peptide
34	CJ	102	GLU	Peptide
34	CJ	160	HIS	Peptide
34	CJ	85	GLU	Peptide
34	CJ	96	GLU	Peptide
2	CL	124	ILE	Peptide
2	CL	133	ILE	Peptide
2	CL	154	LEU	Peptide
2	CL	159	GLU	Peptide
2	CL	160	GLN	Peptide
2	CL	169	VAL	Peptide
2	CL	3	LYS	Peptide

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Mol	Chain	Res	Type	Group
2	CL	4	GLY	Peptide
2	CL	51	SER	Peptide
2	CL	57	VAL	Peptide
2	CL	58	VAL	Peptide
2	CL	6	ASN	Peptide
2	CL	75	PHE	Peptide
2	CL	96	ALA	Peptide
4	CM	103	SER	Peptide
4	CM	127	PHE	Peptide
6	CN	182	GLN	Peptide
6	CN	186	GLY	Peptide
6	CN	28	TRP	Peptide
6	CN	41	ARG	Peptide
6	CN	64	ILE	Peptide
6	CN	66	VAL	Peptide
6	CN	78	GLY	Peptide
1	CO	109	GLY	Peptide
1	CO	111	PRO	Peptide
1	CO	112	SER	Peptide
1	CO	177	LYS	Peptide
1	CO	190	ALA	Peptide
1	CO	191	ALA	Peptide
1	CO	198	ILE	Peptide
1	CO	201	TYR	Peptide
1	CO	202	GLY	Peptide
14	CP	20	PRO	Peptide
14	CP	63	PHE	Peptide
14	CP	9	ASP	Peptide
9	CQ	156	PRO	Peptide
9	CQ	160	HIS	Peptide
9	CQ	163	THR	Peptide
9	CQ	4	ASP	Peptide
9	CQ	5	ILE	Peptide
10	CR	112	SER	Peptide
10	CR	113	LYS	Peptide
10	CR	170	ARG	Peptide
12	CS	118	ARG	Peptide
12	CS	120	ARG	Peptide
12	CS	138	ARG	Peptide
12	CS	15	ARG	Peptide
12	CS	157	ARG	Peptide
12	CS	162	GLY	Peptide

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Mol	Chain	Res	Type	Group
12	CS	163	ASN	Peptide
12	CS	175	TYR	Peptide
12	CS	55	LYS	Peptide
12	CS	67	VAL	Peptide
12	CS	88	SER	Peptide
13	CT	135	PRO	Peptide
13	CT	145	GLU	Peptide
13	CT	147	PRO	Peptide
13	CT	157	PHE	Peptide
13	CT	3	ASN	Peptide
13	CT	4	SER	Peptide
13	CT	54	TYR	Peptide
13	CT	6	GLY	Peptide
76	CU	286	PHE	Peptide
78	CW	60	ARG	Peptide
16	CY	63	LYS	Peptide
16	CY	64	GLY	Peptide
5	Ca	115	ARG	Peptide
5	Ca	144	VAL	Peptide
5	Ca	57	VAL	Peptide
5	Ca	58	GLY	Peptide
5	Ca	98	LYS	Peptide
20	Cb	19	ASN	Peptide
20	Cb	21	ILE	Peptide
20	Cb	3	LYS	Peptide
20	Cb	43	GLN	Peptide
80	Cd	39	ALA	Peptide
24	Ce	14	LYS	Peptide
24	Ce	2	THR	Peptide
24	Ce	5	PRO	Peptide
25	Cf	101	LYS	Peptide
25	Cf	108	PRO	Peptide
25	Cf	137	ARG	Peptide
25	Cf	37	ALA	Peptide
25	Cf	39	VAL	Peptide
25	Cf	42	LYS	Peptide
25	Cf	44	TYR	Peptide
25	Cf	45	LYS	Peptide
25	Cf	46	ARG	Peptide
25	Cf	47	HIS	Peptide
25	Cf	49	ARG	Peptide
79	Cg	72	VAL	Peptide

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Mol	Chain	Res	Type	Group
19	Ch	121	VAL	Peptide
19	Ch	42	SER	Peptide
19	Ch	43	LYS	Peptide
19	Ch	73	PHE	Peptide
19	Ch	84	ARG	Peptide
26	Ci	12	ASN	Peptide
26	Ci	3	VAL	Peptide
26	Ci	37	SER	Peptide
26	Ci	41	ASN	Peptide
26	Ci	43	GLN	Peptide
26	Ci	87	LEU	Peptide
26	Ci	9	ILE	Peptide
27	Ck	39	SER	Peptide
27	Ck	40	ARG	Peptide
30	Cm	124	LYS	Peptide
30	Cm	125	LYS	Peptide
33	Co	26	TYR	Peptide
33	Co	34	GLY	Peptide
33	Co	46	GLN	Peptide
18	Cr	108	LYS	Peptide
18	Cr	25	VAL	Peptide
18	Cr	26	LYS	Peptide
18	Cr	41	SER	Peptide
18	Cr	43	ARG	Peptide
18	Cr	46	GLY	Peptide
18	Cr	50	LYS	Peptide
18	Cr	69	LYS	Peptide
18	Cr	71	GLY	Peptide
18	Cr	72	LYS	Peptide
18	Cr	75	GLN	Peptide
18	Cr	79	LYS	Peptide
18	Cr	80	ASN	Peptide
18	Cr	81	THR	Peptide
18	Cr	86	PHE	Peptide
68	Cz	101	LYS	Peptide
68	Cz	158	GLN	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CO	1668	0	1783	32	0
2	CL	1695	0	1790	41	0
3	CV	998	0	1046	13	0
4	CM	1302	0	1388	41	0
5	Ca	1204	0	1260	40	0
6	CN	1710	0	1778	41	0
7	CI	1785	0	1804	35	0
8	CD	2334	0	2354	52	0
9	CQ	1518	0	1626	45	0
10	CR	1683	0	1827	35	0
11	CA	1935	0	2037	54	0
12	CS	1454	0	1503	42	0
13	CT	1297	0	1364	24	0
14	CP	1505	0	1556	32	0
15	CX	984	0	1058	25	0
16	CY	1078	0	1159	25	0
17	CZ	1115	0	1199	26	0
18	Cr	1051	0	1148	43	0
19	Ch	1015	0	1163	12	0
20	Cb	619	0	650	10	0
21	CB	3287	0	3432	67	0
22	CF	1895	0	2012	34	0
23	Cc	770	0	802	20	0
24	Ce	1110	0	1181	29	0
25	Cf	1244	0	1316	47	0
26	Ci	934	0	1029	19	0
27	Ck	576	0	634	10	0
28	Cl	437	0	483	7	0
29	CC	3109	0	3298	50	0
30	Cm	429	0	472	15	0
31	Cn	236	0	286	3	0
32	Cp	710	0	756	15	0
33	Co	874	0	956	12	0
34	CJ	1468	0	1507	33	0
35	CH	1499	0	1569	34	0
36	CE	1845	0	1981	66	0
37	CG	1936	0	2103	38	0
38	A9	639	0	321	4	0
39	A7	2554	0	1296	26	0
40	A8	2621	0	1327	25	0
41	Ag	2511	0	2438	69	0
42	AU	815	0	871	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	AO	953	0	988	26	0
44	AX	1131	0	1190	24	0
45	AM	924	0	960	27	0
46	Ad	433	0	424	10	0
47	AN	1202	0	1291	17	0
48	AL	1274	0	1351	25	0
49	AR	981	0	1038	25	0
50	AP	1016	0	1086	89	0
51	AB	1798	0	1867	38	0
52	AA	1737	0	1750	44	0
53	AV	617	0	613	17	0
54	AY	1016	0	1073	27	0
55	AZ	608	0	657	133	0
56	Aa	867	0	920	31	0
57	Ab	653	0	680	26	0
58	AD	1782	0	1862	40	0
59	Ae	469	0	503	10	0
60	Af	659	0	695	20	0
61	AJ	1503	0	1620	41	0
62	AE	2054	0	2165	52	0
63	AC	1746	0	1827	37	0
64	AG	1866	0	2029	60	0
65	AH	1566	0	1664	42	0
66	AI	1665	0	1746	29	0
67	AQ	1183	0	1255	52	0
68	Cz	1702	0	1814	45	0
69	A5	77093	0	38445	767	0
70	B2	39355	0	19532	519	0
71	AW	1028	0	1071	19	0
72	AT	1000	0	1037	34	0
73	AK	760	0	757	23	0
74	AF	1481	0	1541	45	0
75	Ac	498	0	525	13	0
76	CU	825	0	853	14	0
77	Cj	704	0	733	14	0
78	CW	503	0	536	6	0
79	Cg	844	0	924	18	0
80	Cd	893	0	918	50	0
81	AS	1117	0	1148	290	0
All	All	216955	0	160651	3163	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (3163) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:B2:1758:A:P	81:AS:37:GLY:HA3	1.59	1.43
55:AZ:49:PHE:HB3	81:AS:6:PRO:C	1.45	1.41
55:AZ:51:LYS:HE3	81:AS:6:PRO:CG	1.49	1.39
55:AZ:48:LEU:HD11	81:AS:11:HIS:NE2	1.28	1.38
55:AZ:51:LYS:CE	81:AS:6:PRO:HG3	1.53	1.35
55:AZ:46:GLN:HA	81:AS:23:LYS:CG	1.55	1.34
50:AP:20:TYR:CE2	81:AS:90:ILE:HG21	1.63	1.33
50:AP:20:TYR:CZ	81:AS:90:ILE:HG21	1.64	1.33
55:AZ:48:LEU:CG	81:AS:7:GLU:OE1	1.75	1.33
50:AP:21:ARG:HB3	81:AS:93:GLY:CA	1.59	1.30
70:B2:1731:U:C4	81:AS:28:ILE:HB	1.66	1.30
55:AZ:49:PHE:N	81:AS:7:GLU:HB2	1.44	1.29
50:AP:20:TYR:O	81:AS:91:ILE:HA	1.11	1.28
70:B2:1740:G:C5'	81:AS:88:LYS:HB3	1.54	1.28
55:AZ:81:SER:OG	81:AS:55:ARG:NH2	1.64	1.27
55:AZ:46:GLN:NE2	81:AS:23:LYS:HA	1.45	1.26
50:AP:20:TYR:O	81:AS:91:ILE:CA	1.84	1.25
70:B2:1695:A:C4	81:AS:82:TRP:NE1	2.08	1.21
70:B2:1758:A:OP1	81:AS:37:GLY:CA	1.89	1.21
70:B2:1758:A:OP1	81:AS:37:GLY:HA3	1.04	1.20
69:A5:3960:U:C5'	80:Cd:20:ARG:HH21	1.53	1.20
70:B2:1695:A:C2	81:AS:82:TRP:CZ2	2.31	1.19
50:AP:21:ARG:HG2	81:AS:90:ILE:O	1.37	1.19
55:AZ:46:GLN:HE21	81:AS:23:LYS:CA	1.56	1.18
70:B2:1731:U:C5	81:AS:28:ILE:HB	1.80	1.17
70:B2:1695:A:C5	81:AS:82:TRP:NE1	2.11	1.16
55:AZ:47:VAL:N	81:AS:23:LYS:HG2	1.60	1.16
55:AZ:48:LEU:HA	81:AS:7:GLU:HG3	1.22	1.16
55:AZ:52:ALA:CB	81:AS:8:LYS:HE2	1.74	1.14
55:AZ:48:LEU:HG	81:AS:7:GLU:OE1	0.99	1.14
70:B2:1758:A:O5'	81:AS:37:GLY:N	1.79	1.14
70:B2:1650:G:OP1	81:AS:136:THR:N	1.80	1.13
70:B2:1740:G:H5'	81:AS:88:LYS:CB	1.79	1.13
70:B2:1695:A:C5	81:AS:82:TRP:CD1	2.36	1.12
70:B2:1758:A:P	81:AS:37:GLY:CA	2.37	1.12
55:AZ:51:LYS:HG2	81:AS:6:PRO:HB3	1.21	1.12
70:B2:1740:G:H1'	81:AS:87:GLN:NE2	1.63	1.12
69:A5:3960:U:H5''	80:Cd:20:ARG:HH21	0.95	1.10
55:AZ:46:GLN:CA	81:AS:23:LYS:HG3	1.81	1.10
55:AZ:52:ALA:CB	81:AS:8:LYS:CE	2.28	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:AP:21:ARG:HB3	81:AS:93:GLY:HA3	1.25	1.09
70:B2:1654:G:OP2	81:AS:141:ARG:NH2	1.85	1.09
50:AP:21:ARG:CG	81:AS:90:ILE:O	1.98	1.09
55:AZ:47:VAL:H	81:AS:23:LYS:HG2	0.99	1.09
50:AP:114:MET:HG2	81:AS:117:ILE:CG2	1.82	1.08
70:B2:1695:A:N7	81:AS:82:TRP:CD1	2.22	1.06
50:AP:114:MET:HG2	81:AS:117:ILE:HG22	1.07	1.06
70:B2:1695:A:N3	81:AS:82:TRP:CZ2	2.23	1.05
70:B2:1736:U:C5'	81:AS:131:VAL:HG22	1.85	1.05
55:AZ:48:LEU:CD1	81:AS:11:HIS:NE2	2.17	1.05
55:AZ:79:ARG:NH1	81:AS:23:LYS:HZ1	1.53	1.05
70:B2:1740:G:C5'	81:AS:88:LYS:CB	2.24	1.05
70:B2:1695:A:H1'	81:AS:83:PHE:CZ	1.91	1.05
55:AZ:52:ALA:HB2	81:AS:8:LYS:HE2	1.08	1.04
70:B2:1695:A:C4	81:AS:82:TRP:CE2	2.45	1.04
70:B2:1740:G:H1'	81:AS:87:GLN:HE21	0.91	1.03
55:AZ:48:LEU:HG	81:AS:7:GLU:CD	1.83	1.03
50:AP:20:TYR:CE2	81:AS:90:ILE:CG2	2.43	1.02
55:AZ:50:ASP:H	81:AS:7:GLU:N	1.58	1.02
55:AZ:47:VAL:N	81:AS:23:LYS:HE2	1.75	1.01
69:A5:3960:U:H5''	80:Cd:20:ARG:NH2	1.76	1.01
55:AZ:49:PHE:H	81:AS:7:GLU:HB2	0.92	1.00
55:AZ:48:LEU:HD11	81:AS:11:HIS:CD2	1.97	1.00
50:AP:21:ARG:CD	81:AS:93:GLY:HA2	1.92	0.99
70:B2:1731:U:C4	81:AS:28:ILE:CB	2.44	0.98
55:AZ:49:PHE:H	81:AS:7:GLU:CB	1.76	0.98
55:AZ:47:VAL:CG2	81:AS:23:LYS:HE2	1.92	0.98
50:AP:21:ARG:HA	81:AS:90:ILE:O	1.65	0.97
55:AZ:46:GLN:CA	81:AS:23:LYS:CG	2.39	0.97
50:AP:21:ARG:HD3	81:AS:93:GLY:HA2	1.46	0.97
55:AZ:52:ALA:HB2	81:AS:8:LYS:CE	1.91	0.97
50:AP:20:TYR:CZ	81:AS:90:ILE:CG2	2.48	0.97
55:AZ:47:VAL:CG2	81:AS:23:LYS:CE	2.43	0.96
55:AZ:49:PHE:HB3	81:AS:6:PRO:O	1.63	0.96
55:AZ:51:LYS:N	81:AS:8:LYS:NZ	2.13	0.96
70:B2:1731:U:C5	81:AS:28:ILE:CB	2.31	0.96
69:A5:3960:U:C5'	80:Cd:20:ARG:NH2	2.26	0.96
55:AZ:49:PHE:N	81:AS:7:GLU:CB	2.30	0.95
50:AP:108:VAL:HG23	81:AS:118:ARG:NH2	1.82	0.95
69:A5:1701:C:H5'	80:Cd:43:ILE:HG21	1.48	0.94
69:A5:3960:U:OP1	80:Cd:118:ASN:ND2	2.01	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:AZ:47:VAL:HG22	81:AS:23:LYS:NZ	1.81	0.93
55:AZ:48:LEU:CD1	81:AS:11:HIS:CD2	2.51	0.93
55:AZ:79:ARG:CZ	81:AS:23:LYS:HZ1	1.81	0.93
70:B2:1695:A:H1'	81:AS:83:PHE:HZ	1.24	0.92
50:AP:21:ARG:CA	81:AS:90:ILE:O	2.16	0.92
50:AP:21:ARG:CB	81:AS:93:GLY:CA	2.48	0.91
69:A5:1698:A:N7	80:Cd:36:LYS:NZ	2.18	0.91
55:AZ:46:GLN:HE21	81:AS:23:LYS:HA	0.76	0.91
55:AZ:49:PHE:CB	81:AS:6:PRO:C	2.41	0.91
55:AZ:81:SER:HG	81:AS:55:ARG:HH21	0.95	0.91
70:B2:1695:A:C5	81:AS:82:TRP:CE2	2.59	0.90
55:AZ:52:ALA:HB3	81:AS:8:LYS:HE3	1.53	0.90
70:B2:1740:G:C1'	81:AS:87:GLN:HE21	1.83	0.90
55:AZ:47:VAL:HG22	81:AS:23:LYS:HZ1	1.33	0.90
55:AZ:51:LYS:HG2	81:AS:6:PRO:CB	2.02	0.90
55:AZ:47:VAL:H	81:AS:23:LYS:CG	1.85	0.90
55:AZ:51:LYS:N	81:AS:8:LYS:HZ3	1.67	0.89
70:B2:1063:G:H1	70:B2:1110:A:HO2'	0.93	0.89
69:A5:1699:A:N6	69:A5:1718:G:N3	2.19	0.88
70:B2:1741:A:OP2	81:AS:88:LYS:NZ	1.89	0.88
55:AZ:47:VAL:HG22	81:AS:23:LYS:CE	2.04	0.87
55:AZ:47:VAL:HG23	81:AS:23:LYS:CD	2.05	0.87
55:AZ:79:ARG:NH1	81:AS:23:LYS:NZ	2.23	0.87
70:B2:1758:A:O5'	81:AS:37:GLY:CA	2.22	0.86
50:AP:21:ARG:CA	81:AS:93:GLY:N	2.33	0.86
70:B2:1736:U:O2'	81:AS:131:VAL:CG1	2.23	0.85
70:B2:1695:A:C2	81:AS:82:TRP:CE2	2.65	0.85
55:AZ:47:VAL:HG23	81:AS:23:LYS:CE	2.05	0.85
70:B2:1740:G:H5'	81:AS:88:LYS:HB3	0.85	0.85
69:A5:1698:A:C8	80:Cd:36:LYS:NZ	2.45	0.84
50:AP:21:ARG:HB3	81:AS:93:GLY:HA2	1.58	0.84
69:A5:546:G:H1	69:A5:756:C:H42	1.21	0.84
55:AZ:48:LEU:HA	81:AS:7:GLU:CG	2.08	0.83
55:AZ:46:GLN:HA	81:AS:23:LYS:HG3	0.85	0.83
55:AZ:79:ARG:CZ	81:AS:23:LYS:NZ	2.41	0.82
50:AP:21:ARG:HA	81:AS:93:GLY:N	1.93	0.82
70:B2:1736:U:H5''	81:AS:131:VAL:HG22	1.61	0.82
69:A5:1172:G:H1	69:A5:1322:U:H3	1.28	0.82
55:AZ:48:LEU:CD1	81:AS:7:GLU:OE1	2.28	0.81
70:B2:1731:U:O4	81:AS:28:ILE:HB	1.80	0.81
70:B2:1757:G:N2	81:AS:85:ASN:O	2.13	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:AZ:47:VAL:HG23	81:AS:23:LYS:HD3	1.63	0.80
50:AP:122:PHE:CD1	81:AS:117:ILE:O	2.35	0.80
69:A5:554:U:H3	69:A5:658:A:H61	1.29	0.80
69:A5:3593:A:H5'	80:Cd:35:PHE:CZ	2.16	0.80
70:B2:1651:C:OP2	81:AS:136:THR:OG1	1.97	0.80
70:B2:1695:A:C2	81:AS:82:TRP:CH2	2.70	0.80
55:AZ:47:VAL:CA	81:AS:23:LYS:HE2	2.11	0.79
70:B2:1695:A:C6	81:AS:82:TRP:CD2	2.71	0.79
70:B2:1695:A:C8	81:AS:82:TRP:NE1	2.50	0.78
70:B2:1649:U:H1'	81:AS:135:HIS:HD2	1.47	0.78
70:B2:1739:U:O2'	81:AS:87:GLN:O	2.00	0.78
50:AP:108:VAL:HG23	81:AS:118:ARG:HH21	1.49	0.78
69:A5:3415:U:H3	69:A5:3471:A:H61	1.31	0.78
80:Cd:39:ALA:HB1	80:Cd:42:ALA:H	1.46	0.78
69:A5:1177:U:H3	69:A5:1317:A:H61	1.30	0.78
2:CL:74:GLY:HA2	2:CL:98:ASP:HB3	1.67	0.77
55:AZ:46:GLN:CA	81:AS:23:LYS:HG2	2.14	0.77
50:AP:20:TYR:O	81:AS:90:ILE:O	2.02	0.77
12:CS:163:ASN:HB3	12:CS:165:LYS:H	1.50	0.76
50:AP:122:PHE:HD1	81:AS:117:ILE:O	1.67	0.76
69:A5:1198:U:H3	69:A5:1312:G:H22	1.31	0.76
50:AP:121:GLU:O	81:AS:119:SER:HA	1.85	0.76
55:AZ:49:PHE:HB3	81:AS:6:PRO:CA	2.16	0.76
55:AZ:47:VAL:N	81:AS:23:LYS:CG	2.45	0.75
70:B2:1695:A:C6	81:AS:82:TRP:CE2	2.75	0.74
24:Ce:92:ARG:HD3	36:CE:76:LYS:HA	1.70	0.74
69:A5:3960:U:H4'	80:Cd:20:ARG:NH2	2.03	0.74
50:AP:20:TYR:O	81:AS:90:ILE:C	2.30	0.74
50:AP:21:ARG:HG2	81:AS:90:ILE:C	2.13	0.74
55:AZ:47:VAL:N	81:AS:23:LYS:CE	2.49	0.74
55:AZ:47:VAL:HG22	81:AS:23:LYS:HE2	1.67	0.73
55:AZ:52:ALA:HB3	81:AS:8:LYS:CE	2.08	0.73
27:Ck:9:LYS:HZ1	27:Ck:16:ARG:HH22	1.36	0.73
64:AG:210:TYR:HB3	64:AG:213:LEU:HB2	1.70	0.73
1:CO:203:TYR:HB2	4:CM:97:ASN:HD21	1.53	0.73
55:AZ:49:PHE:CB	81:AS:6:PRO:O	2.36	0.73
70:B2:1695:A:C8	81:AS:82:TRP:CD1	2.75	0.73
55:AZ:46:GLN:C	81:AS:23:LYS:HG2	2.14	0.73
56:Aa:2:THR:HB	70:B2:1230:A:H5''	1.70	0.73
70:B2:1651:C:H2'	81:AS:136:THR:O	1.88	0.73
11:CA:9:ARG:NH2	69:A5:1112:G:N7	2.37	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:AT:38:LYS:NZ	81:AS:43:ILE:HD11	2.04	0.72
69:A5:3922:G:H22	69:A5:3931:C:H42	1.36	0.72
12:CS:163:ASN:ND2	69:A5:3758:G:N7	2.37	0.72
21:CB:268:ARG:NH1	69:A5:2770:C:O2'	2.23	0.72
50:AP:20:TYR:O	81:AS:91:ILE:N	2.23	0.72
50:AP:21:ARG:HA	81:AS:92:ASP:N	2.05	0.72
1:CO:66:VAL:HG11	21:CB:261:ARG:HB2	1.72	0.71
50:AP:21:ARG:HB3	81:AS:93:GLY:N	2.04	0.71
66:AI:180:ARG:HE	66:AI:183:GLN:HG3	1.55	0.71
35:CH:23:ARG:NH2	69:A5:3726:U:O2'	2.23	0.71
50:AP:114:MET:CG	81:AS:117:ILE:HG22	2.03	0.71
43:AO:34:TYR:HB3	43:AO:41:PHE:HB2	1.73	0.71
56:Aa:15:ARG:NH2	70:B2:1022:A:N7	2.38	0.71
69:A5:3593:A:H5'	80:Cd:35:PHE:CE1	2.25	0.71
35:CH:23:ARG:HH21	69:A5:3729:A:H1'	1.56	0.71
69:A5:2593:A:H61	69:A5:2608:G:H22	1.38	0.71
39:A7:14:C:H42	39:A7:65:C:H42	1.38	0.70
70:B2:1695:A:N9	81:AS:82:TRP:NE1	2.33	0.70
50:AP:21:ARG:CB	81:AS:93:GLY:N	2.55	0.70
50:AP:21:ARG:CB	81:AS:90:ILE:O	2.39	0.70
69:A5:2909:A:N1	69:A5:3126:C:N4	2.40	0.70
50:AP:21:ARG:HA	81:AS:93:GLY:H	1.56	0.70
55:AZ:46:GLN:NE2	81:AS:23:LYS:CA	2.33	0.70
69:A5:1701:C:H5'	80:Cd:43:ILE:CG2	2.21	0.70
69:A5:557:G:H1	69:A5:655:C:H42	1.39	0.70
69:A5:927:A:N6	69:A5:973:G:N7	2.40	0.70
70:B2:1695:A:N3	81:AS:82:TRP:CE2	2.56	0.70
55:AZ:46:GLN:CD	81:AS:23:LYS:HA	2.15	0.70
69:A5:2646:U:H3	69:A5:2650:G:H22	1.38	0.70
55:AZ:47:VAL:HB	81:AS:55:ARG:HD2	1.74	0.69
70:B2:1262:C:OP1	81:AS:134:GLN:HG3	1.90	0.69
70:B2:1319:A:N7	70:B2:1321:A:N6	2.39	0.69
4:CM:4:GLU:HB2	12:CS:153:PRO:HB3	1.72	0.69
70:B2:1737:U:OP2	81:AS:132:ARG:NH1	2.26	0.69
70:B2:1263:U:OP2	81:AS:135:HIS:ND1	2.20	0.69
50:AP:108:VAL:CG2	81:AS:118:ARG:NH2	2.55	0.69
69:A5:1806:G:N2	69:A5:1809:A:N1	2.40	0.69
69:A5:558:C:H42	69:A5:654:G:H1	1.41	0.69
69:A5:3784:C:H42	69:A5:3827:G:H1	1.39	0.69
70:B2:1740:G:O4'	81:AS:88:LYS:HB2	1.73	0.69
65:AH:186:GLU:HG3	65:AH:188:PRO:HD3	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:Cd:16:GLU:HG2	80:Cd:99:LEU:HD11	1.75	0.69
69:A5:592:G:H21	69:A5:3747:U:H5'	1.58	0.69
35:CH:41:LEU:HD21	35:CH:71:VAL:HG21	1.76	0.68
69:A5:2517:A:HO2'	77:Cj:2:THR:N	1.91	0.68
55:AZ:48:LEU:HD12	81:AS:11:HIS:CD2	2.28	0.68
69:A5:3361:U:H2'	69:A5:3362:G:H8	1.59	0.68
55:AZ:47:VAL:HB	81:AS:23:LYS:O	1.93	0.68
2:CL:163:VAL:H	2:CL:164:VAL:HG13	1.59	0.68
37:CG:63:PRO:HB3	69:A5:1801:U:H2'	1.75	0.68
64:AG:2:LYS:HB2	64:AG:108:VAL:HG22	1.76	0.68
6:CN:15:GLN:NE2	69:A5:312:U:OP2	2.27	0.68
55:AZ:47:VAL:CG2	81:AS:23:LYS:NZ	2.56	0.68
55:AZ:68:THR:H	55:AZ:71:VAL:HG12	1.59	0.68
69:A5:3840:G:N3	69:A5:3843:U:N3	2.42	0.68
69:A5:3960:U:C4'	80:Cd:20:ARG:NH2	2.57	0.68
73:AK:23:ALA:HB3	73:AK:65:TYR:HB3	1.75	0.68
17:CZ:17:ARG:NH1	69:A5:1946:G:N7	2.42	0.67
32:Cp:56:SER:HB2	32:Cp:63:THR:HG23	1.76	0.67
10:CR:164:GLN:HA	10:CR:167:ARG:HE	1.58	0.67
24:Ce:127:ARG:NH2	69:A5:1634:A:OP1	2.25	0.67
42:AU:20:HIS:HE2	42:AU:97:SER:HG	1.38	0.67
61:AJ:172:GLY:HA3	61:AJ:175:LYS:H	1.56	0.67
50:AP:21:ARG:CD	81:AS:90:ILE:CA	2.70	0.67
55:AZ:50:ASP:H	81:AS:7:GLU:H	1.36	0.67
69:A5:3569:C:OP2	69:A5:3571:C:N4	2.27	0.67
70:B2:1399:A:H61	70:B2:1417:G:H4'	1.58	0.67
72:AT:38:LYS:HZ1	81:AS:43:ILE:HD11	1.57	0.67
35:CH:57:LYS:HE2	35:CH:64:GLU:HB3	1.74	0.67
55:AZ:47:VAL:HB	81:AS:55:ARG:CD	2.25	0.67
1:CO:24:VAL:HG21	1:CO:122:VAL:HG11	1.75	0.67
5:Ca:36:ALA:HB2	69:A5:99:A:H4'	1.77	0.67
9:CQ:156:PRO:HB3	9:CQ:188:LYS:HB2	1.74	0.67
36:CE:21:PRO:HA	36:CE:32:ARG:HD2	1.76	0.67
11:CA:221:LYS:HD2	11:CA:233:ARG:HH22	1.59	0.67
55:AZ:54:TYR:HA	55:AZ:57:LEU:HB2	1.75	0.67
70:B2:1736:U:C4'	81:AS:131:VAL:HG22	2.07	0.67
70:B2:1750:U:C2	81:AS:124:ARG:HD3	2.30	0.67
56:Aa:99:LEU:H	56:Aa:100:ARG:HE	1.43	0.67
70:B2:958:G:H1	70:B2:1043:U:H3	1.41	0.67
14:CP:126:ARG:HD2	14:CP:140:MET:HE1	1.77	0.66
56:Aa:38:LYS:HB2	56:Aa:71:LEU:HB2	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:AP:21:ARG:CD	81:AS:90:ILE:HA	2.18	0.66
69:A5:1910:C:H3'	69:A5:1924:A:H4'	1.76	0.66
14:CP:131:ARG:NH2	69:A5:2734:A:N3	2.42	0.66
69:A5:3364:C:H2'	69:A5:3365:G:H8	1.60	0.66
5:Ca:39:MET:O	5:Ca:43:ARG:NH1	2.27	0.66
11:CA:82:MET:HG3	11:CA:86:GLN:HE21	1.61	0.66
69:A5:2155:A:H2	69:A5:2169:U:H3	1.43	0.66
42:AU:53:LYS:HE2	70:B2:1431:A:H4'	1.78	0.66
43:AO:99:ALA:HB3	43:AO:101:GLY:H	1.59	0.66
22:CF:58:GLU:O	22:CF:62:ASN:ND2	2.29	0.66
68:Cz:24:LYS:HG2	68:Cz:26:ARG:H	1.61	0.66
20:Cb:76:LEU:HD21	69:A5:1293:A:H3'	1.78	0.66
33:Co:61:LYS:NZ	69:A5:3292:C:N3	2.43	0.66
70:B2:1650:G:P	81:AS:136:THR:H	2.14	0.66
11:CA:234:LYS:HG2	11:CA:238:ILE:HD12	1.77	0.66
35:CH:23:ARG:NH2	69:A5:3728:A:OP1	2.28	0.66
53:AV:78:ILE:HG22	53:AV:79:VAL:HG23	1.76	0.66
78:CW:56:ARG:HE	78:CW:61:LYS:HD2	1.61	0.66
50:AP:98:GLY:HA2	50:AP:107:GLN:HA	1.77	0.65
64:AG:121:ILE:HG22	64:AG:123:GLY:H	1.60	0.65
70:B2:54:C:H2'	70:B2:55:A:H8	1.61	0.65
69:A5:2516:U:OP2	69:A5:2521:A:N6	2.30	0.65
20:Cb:2:ALA:HB2	69:A5:3350:U:H5''	1.79	0.65
50:AP:20:TYR:CD2	81:AS:90:ILE:CG2	2.79	0.65
69:A5:2924:A:H61	69:A5:2993:G:H1	1.43	0.65
70:B2:1695:A:C4	81:AS:82:TRP:CZ2	2.81	0.65
74:AF:216:ILE:HA	74:AF:219:LYS:HD2	1.79	0.65
11:CA:146:THR:HG1	11:CA:160:SER:HG	1.45	0.65
12:CS:157:ARG:HH11	69:A5:3753:A:H2'	1.60	0.65
40:A8:70:A:N6	40:A8:85:G:O2'	2.29	0.65
63:AC:242:MET:HG3	63:AC:244:LEU:H	1.60	0.65
67:AQ:13:GLN:NE2	70:B2:1428:A:OP1	2.30	0.65
40:A8:8:A:H2'	40:A8:9:G:H8	1.62	0.65
55:AZ:46:GLN:HG2	81:AS:23:LYS:CB	2.27	0.65
15:CX:159:ARG:HH12	37:CG:58:ARG:HH11	1.43	0.65
69:A5:122:C:H1'	69:A5:159:G:H1	1.62	0.65
70:B2:1758:A:P	81:AS:37:GLY:N	2.66	0.65
9:CQ:173:LYS:NZ	69:A5:93:G:N7	2.44	0.65
12:CS:175:TYR:O	69:A5:3730:G:N2	2.29	0.65
21:CB:165:HIS:HB3	21:CB:180:VAL:HG12	1.78	0.65
55:AZ:47:VAL:HG13	55:AZ:79:ARG:HE	1.62	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:AH:7:ILE:HG23	65:AH:8:ILE:HG12	1.79	0.65
23:Cc:34:THR:HG23	23:Cc:95:SER:HB3	1.78	0.65
51:AB:137:LEU:HB3	51:AB:222:LYS:HB2	1.79	0.65
61:AJ:108:GLU:O	61:AJ:114:GLN:NE2	2.30	0.65
69:A5:119:G:H2'	69:A5:283:A:H1'	1.79	0.65
4:CM:143:LEU:HD22	69:A5:3820:C:H41	1.62	0.64
52:AA:156:TYR:HA	53:AV:60:ARG:HB3	1.79	0.64
69:A5:3418:U:H3	69:A5:3468:G:H1	1.45	0.64
26:Ci:39:LEU:O	69:A5:284:A:N6	2.30	0.64
34:CJ:123:LYS:HD3	81:AS:12:ILE:HG21	1.78	0.64
41:Ag:254:GLY:O	41:Ag:284:GLN:NE2	2.30	0.64
53:AV:56:CYS:SG	53:AV:57:GLY:N	2.70	0.64
43:AO:126:ILE:H	56:Aa:56:ALA:HB1	1.63	0.64
69:A5:1112:G:H21	69:A5:1115:A:H62	1.46	0.64
69:A5:2006:U:H3	69:A5:2066:G:H1	1.44	0.64
1:CO:133:SER:HB3	69:A5:3727:A:H2'	1.79	0.64
10:CR:181:LYS:HZ3	10:CR:184:LEU:HD12	1.62	0.64
44:AX:88:ASP:HB2	70:B2:576:G:H4'	1.79	0.64
72:AT:38:LYS:CE	81:AS:43:ILE:HD11	2.28	0.64
66:AI:61:GLU:HG2	66:AI:62:THR:HG23	1.79	0.64
67:AQ:52:LYS:HB3	74:AF:75:LEU:HB2	1.77	0.64
69:A5:3721:C:N4	69:A5:3761:U:O4	2.30	0.64
11:CA:117:GLU:HG2	11:CA:124:GLY:H	1.62	0.64
21:CB:220:VAL:HG22	21:CB:278:THR:HG23	1.80	0.64
22:CF:167:ARG:NH2	69:A5:1317:A:OP2	2.31	0.64
68:Cz:48:ARG:NH2	68:Cz:157:PHE:O	2.29	0.64
80:Cd:30:VAL:HG21	80:Cd:39:ALA:HB2	1.80	0.64
4:CM:71:ARG:NH1	69:A5:632:A:OP2	2.30	0.64
49:AR:53:TYR:O	49:AR:56:HIS:ND1	2.31	0.64
68:Cz:48:ARG:NH1	68:Cz:49:PHE:O	2.31	0.64
69:A5:2062:A:H4'	69:A5:2063:A:H5''	1.79	0.64
70:B2:1808:G:N3	75:Ac:20:GLN:NE2	2.46	0.64
80:Cd:51:GLU:HG2	80:Cd:57:THR:HA	1.79	0.64
6:CN:50:ARG:NH2	69:A5:286:A:OP1	2.28	0.64
65:AH:132:VAL:HG13	65:AH:135:ALA:HB2	1.80	0.64
69:A5:122:C:O2	69:A5:159:G:N2	2.31	0.64
69:A5:3891:U:H1'	69:A5:3892:A:H5''	1.79	0.64
70:B2:1757:G:OP1	81:AS:39:ARG:HD2	1.96	0.64
13:CT:17:ARG:HG2	69:A5:3232:G:H5''	1.80	0.63
49:AR:23:ARG:NH1	58:AD:217:GLU:OE1	2.31	0.63
42:AU:22:ILE:HB	42:AU:93:LEU:HB3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:AP:20:TYR:CD2	81:AS:90:ILE:HG23	2.33	0.63
69:A5:758:A:H5''	69:A5:3840:G:H5'	1.80	0.63
4:CM:147:ARG:HH22	69:A5:3820:C:H42	1.46	0.63
69:A5:477:C:OP1	69:A5:481:A:N6	2.31	0.63
69:A5:3917:G:H21	69:A5:3936:A:H2	1.45	0.63
49:AR:22:THR:HG23	49:AR:23:ARG:HE	1.63	0.63
50:AP:109:GLU:N	81:AS:118:ARG:HH22	1.97	0.63
55:AZ:50:ASP:N	81:AS:7:GLU:N	2.39	0.63
70:B2:1651:C:OP2	81:AS:136:THR:CG2	2.46	0.63
22:CF:97:ARG:NH2	22:CF:100:GLY:O	2.31	0.63
69:A5:1965:A:H2'	69:A5:1966:A:H8	1.63	0.63
69:A5:3737:A:N6	69:A5:3743:U:O4	2.31	0.63
70:B2:1821:G:H21	70:B2:1960:A:H8	1.46	0.63
10:CR:96:MET:SD	10:CR:100:ARG:NH2	2.67	0.63
55:AZ:48:LEU:HG	81:AS:7:GLU:HB3	1.78	0.63
69:A5:652:G:N2	69:A5:655:C:OP2	2.30	0.63
6:CN:14:LYS:HE2	69:A5:287:G:H5''	1.81	0.63
9:CQ:17:GLU:OE2	9:CQ:26:ARG:NH1	2.32	0.63
18:Cr:81:THR:OG1	29:CC:149:GLY:O	2.17	0.63
64:AG:220:GLU:HA	64:AG:223:ALA:HB3	1.80	0.63
66:AI:206:SER:O	69:A5:2472:A:N6	2.30	0.63
69:A5:168:G:H1	69:A5:279:U:H3	1.44	0.63
70:B2:453:C:H42	70:B2:463:G:H1	1.47	0.63
21:CB:229:LYS:H	21:CB:234:ARG:HH22	1.46	0.63
41:Ag:300:PHE:HB3	41:Ag:308:ILE:HD11	1.80	0.63
70:B2:1295:U:H3	70:B2:1648:C:H5	1.47	0.63
4:CM:117:ARG:NH1	69:A5:3768:C:OP2	2.31	0.63
21:CB:395:ASP:HA	21:CB:398:LYS:HG2	1.80	0.63
55:AZ:47:VAL:HG23	81:AS:23:LYS:HE2	1.71	0.63
62:AE:49:ARG:NH1	70:B2:452:U:OP1	2.32	0.63
64:AG:94:ARG:NH2	70:B2:1865:G:OP1	2.32	0.63
70:B2:50:C:N4	70:B2:430:A:OP2	2.30	0.63
70:B2:1695:A:C6	81:AS:82:TRP:CG	2.87	0.63
16:CY:45:ARG:NH2	69:A5:203:A:OP2	2.32	0.62
21:CB:233:SER:O	21:CB:272:LYS:NZ	2.31	0.62
30:Cm:96:CYS:SG	30:Cm:97:ARG:N	2.72	0.62
41:Ag:19:THR:H	41:Ag:35:SER:HA	1.64	0.62
41:Ag:196:LEU:HA	41:Ag:212:GLY:HA2	1.81	0.62
69:A5:1889:A:O2'	69:A5:1891:U:OP2	2.16	0.62
70:B2:1397:U:H3	70:B2:1402:U:H3	1.47	0.62
24:Ce:15:ARG:NH2	24:Ce:52:TYR:OH	2.31	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:Cl:8:ARG:NH2	40:A8:109:U:OP2	2.32	0.62
69:A5:73:U:O2'	69:A5:105:A:O2'	2.16	0.62
69:A5:1450:U:H3	69:A5:1478:A:H62	1.45	0.62
21:CB:213:GLN:NE2	21:CB:285:TYR:O	2.31	0.62
39:A7:75:G:N2	39:A7:100:A:OP2	2.31	0.62
64:AG:176:LYS:HG3	70:B2:65:A:H3'	1.82	0.62
58:AD:61:LEU:HA	58:AD:68:ILE:HB	1.81	0.62
68:Cz:119:GLN:HG2	68:Cz:123:LEU:HD23	1.82	0.62
55:AZ:46:GLN:NE2	81:AS:22:GLY:O	2.32	0.62
69:A5:555:U:H3	69:A5:657:G:H22	1.46	0.62
70:B2:1187:U:H1'	70:B2:1188:G:H5'	1.81	0.62
57:Ab:56:CYS:SG	57:Ab:57:ALA:N	2.72	0.62
62:AE:131:LEU:HG	70:B2:247:G:H1'	1.81	0.62
63:AC:179:ILE:HB	63:AC:206:TYR:HB2	1.82	0.62
80:Cd:72:LYS:O	80:Cd:76:SER:OG	2.16	0.62
14:CP:102:ALA:HB1	14:CP:107:LEU:HB2	1.80	0.62
56:Aa:7:ASN:ND2	70:B2:1021:A:N7	2.43	0.62
21:CB:104:ASN:HB3	69:A5:3682:U:H5'	1.82	0.62
55:AZ:50:ASP:C	81:AS:8:LYS:NZ	2.58	0.62
69:A5:932:G:N2	69:A5:972:U:O2	2.32	0.62
69:A5:3795:G:H22	69:A5:3814:U:H3	1.47	0.62
1:CO:118:ARG:NH1	1:CO:119:ARG:O	2.32	0.62
7:CI:3:ARG:NH1	7:CI:63:GLU:OE2	2.33	0.62
29:CC:45:GLN:HG3	69:A5:1667:U:H4'	1.82	0.62
5:Ca:126:LYS:HG2	5:Ca:146:LEU:HB2	1.82	0.62
17:CZ:47:ASP:HB3	17:CZ:69:LYS:HG2	1.80	0.62
33:Co:69:ARG:HD3	33:Co:78:ARG:HD2	1.81	0.62
2:CL:160:GLN:O	2:CL:162:ALA:N	2.33	0.61
7:CI:199:TYR:HB3	7:CI:200:ARG:HG2	1.82	0.61
36:CE:170:ARG:HB2	69:A5:3840:G:H5''	1.82	0.61
70:B2:213:G:OP1	70:B2:215:C:N4	2.33	0.61
8:CD:17:GLN:NE2	13:CT:22:HIS:O	2.30	0.61
49:AR:94:ASP:HB2	49:AR:114:ILE:HG21	1.81	0.61
50:AP:67:LYS:HZ2	50:AP:76:PRO:HG2	1.64	0.61
70:B2:1671:U:H3'	72:AT:56:ARG:HH21	1.65	0.61
29:CC:116:ARG:NH2	29:CC:117:LYS:O	2.34	0.61
37:CG:86:HIS:ND1	37:CG:88:PHE:O	2.30	0.61
44:AX:101:LEU:HD23	44:AX:124:LYS:HG3	1.82	0.61
69:A5:1713:U:OP1	69:A5:1755:U:O2'	2.17	0.61
70:B2:1301:G:O2'	70:B2:1331:A:N6	2.33	0.61
70:B2:1651:C:OP2	81:AS:136:THR:HG21	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:B2:1662:C:H4'	70:B2:1732:G:H21	1.64	0.61
4:CM:133:ARG:HD3	69:A5:3813:C:H4'	1.83	0.61
8:CD:30:TYR:HA	8:CD:33:ARG:HB3	1.82	0.61
32:Cp:46:SER:OG	32:Cp:57:CYS:SG	2.57	0.61
51:AB:106:MET:HG3	51:AB:191:LEU:HD13	1.82	0.61
69:A5:3918:A:N6	69:A5:3935:G:O2'	2.30	0.61
74:AF:48:ARG:HH12	74:AF:124:GLU:HB3	1.65	0.61
16:CY:46:SER:OG	69:A5:247:C:OP1	2.19	0.61
25:Cf:88:VAL:O	25:Cf:156:ARG:NH1	2.33	0.61
43:AO:52:THR:HG21	70:B2:982:G:H21	1.65	0.61
52:AA:145:ILE:HG13	52:AA:159:ILE:H	1.64	0.61
69:A5:3676:C:H3'	69:A5:3677:U:H2'	1.82	0.61
70:B2:826:U:H3	70:B2:892:A:H61	1.49	0.61
4:CM:101:ARG:NH2	69:A5:3760:A:OP1	2.34	0.61
10:CR:112:SER:OG	10:CR:113:LYS:N	2.33	0.61
32:Cp:17:ARG:NH1	69:A5:1060:G:OP1	2.33	0.61
55:AZ:46:GLN:HG2	81:AS:23:LYS:HA	1.81	0.61
69:A5:1:U:O2	69:A5:7:A:N6	2.30	0.61
32:Cp:4:ARG:NH1	69:A5:1037:A:OP2	2.33	0.61
46:Ad:50:ILE:HD13	58:AD:18:ILE:HG22	1.81	0.61
69:A5:868:A:N6	69:A5:874:G:OP1	2.31	0.61
70:B2:1960:A:H2	70:B2:1963:G:H1	1.49	0.61
16:CY:52:ASP:HB2	16:CY:110:LYS:HG3	1.81	0.61
22:CF:53:ASN:OD1	22:CF:189:GLN:NE2	2.34	0.61
58:AD:198:ASN:HB3	58:AD:200:ILE:HA	1.83	0.61
69:A5:879:U:O2	69:A5:880:A:N6	2.34	0.61
7:Cl:4:ARG:NH1	69:A5:3360:G:O2'	2.34	0.61
18:Cr:115:LEU:HD13	36:CE:72:LYS:HB3	1.82	0.61
35:CH:31:ARG:NH1	35:CH:147:ASN:OD1	2.34	0.61
69:A5:2066:G:N2	79:Cg:26:PRO:O	2.33	0.61
69:A5:3608:G:N2	69:A5:3945:A:O2'	2.33	0.61
70:B2:126:G:H1	70:B2:178:A:H62	1.49	0.61
22:CF:108:VAL:HG23	22:CF:139:ALA:HA	1.83	0.61
39:A7:22:A:H1'	39:A7:120:U:H1'	1.83	0.61
58:AD:192:LEU:HD13	58:AD:194:TYR:HB2	1.82	0.61
62:AE:100:ARG:HB2	62:AE:114:ILE:HD13	1.82	0.61
66:AI:116:HIS:O	66:AI:154:ARG:NH1	2.34	0.61
69:A5:677:G:H22	69:A5:744:U:H3	1.49	0.61
4:CM:71:ARG:HH22	69:A5:632:A:H5'	1.66	0.60
8:CD:16:TYR:O	39:A7:11:A:N6	2.32	0.60
70:B2:151:G:O6	70:B2:157:C:N4	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:B2:655:A:N7	70:B2:704:U:N3	2.49	0.60
70:B2:1869:C:H42	70:B2:1919:U:H3	1.47	0.60
2:CL:182:LEU:HG	5:Ca:147:LEU:HD21	1.83	0.60
37:CG:51:GLN:OE1	37:CG:54:ARG:NH2	2.34	0.60
58:AD:98:LEU:HG	58:AD:193:PRO:HD3	1.83	0.60
74:AF:144:ASN:ND2	74:AF:207:ALA:O	2.34	0.60
76:CU:276:ASN:ND2	76:CU:282:GLU:OE1	2.34	0.60
4:CM:144:LYS:HZ3	69:A5:3819:C:H42	1.50	0.60
11:CA:1:MET:SD	69:A5:1108:G:O2'	2.59	0.60
41:Ag:245:ASN:ND2	41:Ag:297:GLN:OE1	2.34	0.60
49:AR:73:LEU:HA	49:AR:76:GLU:HB2	1.84	0.60
52:AA:52:GLY:HA2	52:AA:55:TRP:HD1	1.66	0.60
29:CC:238:LEU:HD22	29:CC:243:LEU:HD11	1.83	0.60
42:AU:32:ARG:NH1	42:AU:35:GLU:OE2	2.34	0.60
61:AJ:6:ILE:HG13	61:AJ:9:VAL:HG22	1.83	0.60
73:AK:25:LYS:HA	73:AK:41:LEU:HD21	1.83	0.60
19:Ch:3:LYS:HB2	40:A8:81:A:H1'	1.81	0.60
25:Cf:70:GLN:NE2	69:A5:1379:U:OP1	2.33	0.60
41:Ag:197:ASN:HD21	41:Ag:237:ILE:HG13	1.66	0.60
70:B2:1580:G:H21	70:B2:1603:G:H1	1.48	0.60
2:CL:168:GLU:HG2	5:Ca:98:LYS:HG3	1.84	0.60
8:CD:95:TYR:N	39:A7:47:C:OP1	2.34	0.60
34:CJ:57:LYS:HB3	34:CJ:70:ASN:HA	1.83	0.60
57:Ab:47:PHE:HB3	57:Ab:50:ALA:HA	1.84	0.60
69:A5:1637:U:H2'	69:A5:1638:G:H8	1.65	0.60
8:CD:261:SER:O	39:A7:119:C:N4	2.35	0.60
21:CB:300:LYS:HB3	21:CB:311:ASP:HB2	1.84	0.60
24:Ce:97:GLU:HG3	24:Ce:122:THR:HB	1.84	0.60
28:Cl:42:ARG:NH2	69:A5:1737:U:OP1	2.33	0.60
64:AG:202:ALA:HA	64:AG:205:GLU:HB3	1.84	0.60
10:CR:173:ARG:O	10:CR:176:ARG:NH2	2.34	0.60
18:Cr:75:GLN:HG3	18:Cr:83:ARG:HG2	1.83	0.60
41:Ag:45:LEU:HA	41:Ag:54:GLY:HA3	1.83	0.60
70:B2:1292:A:OP1	70:B2:1648:C:N4	2.34	0.60
4:CM:143:LEU:HD21	69:A5:3821:G:H1'	1.84	0.60
25:Cf:1:MET:N	69:A5:646:G:OP1	2.35	0.60
48:AL:64:ARG:HD2	70:B2:113:G:H1'	1.84	0.60
16:CY:11:ARG:HD2	69:A5:237:G:H5''	1.83	0.60
54:AY:103:GLN:HB2	54:AY:105:ARG:H	1.67	0.60
55:AZ:47:VAL:CB	81:AS:55:ARG:HD2	2.29	0.60
64:AG:216:GLN:HA	64:AG:219:LYS:HG2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:A5:81:A:H61	69:A5:341:A:H61	1.48	0.60
69:A5:3838:A:OP1	69:A5:3840:G:N2	2.34	0.60
70:B2:1649:U:C1'	81:AS:135:HIS:HD2	2.15	0.60
6:CN:12:ARG:HH12	69:A5:314:A:H62	1.49	0.59
12:CS:118:ARG:O	12:CS:120:ARG:NH1	2.34	0.59
48:AL:4:GLN:NE2	48:AL:10:GLN:O	2.35	0.59
55:AZ:85:ARG:NH2	81:AS:53:THR:OG1	2.35	0.59
69:A5:889:G:H1	69:A5:899:G:H1	1.50	0.59
70:B2:1673:U:O4	72:AT:82:ARG:NH2	2.35	0.59
70:B2:1883:U:O2	70:B2:1903:G:N1	2.34	0.59
36:CE:158:LYS:NZ	36:CE:161:GLU:OE2	2.36	0.59
42:AU:95:SER:HB3	42:AU:99:ILE:HD11	1.83	0.59
48:AL:65:ILE:O	70:B2:251:G:N2	2.30	0.59
5:Ca:50:HIS:ND1	9:CQ:175:GLU:OE2	2.35	0.59
6:CN:64:ILE:HD13	6:CN:102:ALA:HB1	1.83	0.59
22:CF:218:ASN:O	69:A5:1548:C:O2'	2.18	0.59
30:Cm:95:ILE:HD11	30:Cm:124:LYS:HD3	1.85	0.59
49:AR:31:ASN:HA	49:AR:34:ILE:HG12	1.83	0.59
58:AD:68:ILE:HD11	58:AD:88:LEU:HB2	1.82	0.59
69:A5:522:G:N2	69:A5:523:C:O2	2.34	0.59
69:A5:936:U:O4	69:A5:967:C:N4	2.35	0.59
69:A5:1228:C:H41	69:A5:1245:C:H41	1.49	0.59
69:A5:1260:A:N6	69:A5:3178:G:O2'	2.26	0.59
37:CG:58:ARG:NH1	38:A9:24:G:N7	2.50	0.59
50:AP:43:ARG:NH2	70:B2:1748:A:O2'	2.34	0.59
2:CL:27:GLN:NE2	69:A5:834:G:OP2	2.35	0.59
12:CS:76:LYS:NZ	12:CS:100:LEU:O	2.36	0.59
36:CE:44:LEU:O	69:A5:681:G:N2	2.36	0.59
51:AB:57:ILE:HG22	51:AB:59:SER:H	1.67	0.59
68:Cz:24:LYS:NZ	68:Cz:28:PHE:O	2.36	0.59
69:A5:1785:G:N2	69:A5:2548:G:OP1	2.33	0.59
69:A5:1876:G:OP1	79:Cg:58:ARG:NH2	2.35	0.59
69:A5:1951:C:OP2	79:Cg:74:ARG:NH2	2.31	0.59
69:A5:2528:A:N6	69:A5:2565:G:O2'	2.33	0.59
69:A5:2529:G:O2'	69:A5:2567:U:OP1	2.19	0.59
70:B2:1367:C:H2'	70:B2:1368:G:H8	1.68	0.59
4:CM:133:ARG:NH1	69:A5:3813:C:O2'	2.36	0.59
52:AA:47:ASN:HD22	52:AA:150:THR:HG21	1.68	0.59
69:A5:1936:U:OP2	69:A5:1938:C:N4	2.34	0.59
69:A5:2811:G:H22	69:A5:3128:U:H3	1.49	0.59
19:Ch:34:ALA:HA	19:Ch:37:THR:HG22	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:Ad:30:LEU:O	70:B2:1287:G:N2	2.35	0.59
54:AY:111:ARG:HH21	54:AY:114:ARG:HH12	1.51	0.59
69:A5:209:U:H3	69:A5:217:G:H1	1.50	0.59
69:A5:1951:C:N4	79:Cg:73:SER:OG	2.36	0.59
7:CI:189:ARG:NH2	7:CI:202:GLU:OE2	2.35	0.59
61:AJ:177:LYS:HA	61:AJ:180:LYS:HB2	1.85	0.59
69:A5:1137:G:H22	69:A5:1160:U:H5''	1.68	0.59
69:A5:1880:A:O2'	69:A5:2008:U:O2	2.21	0.59
70:B2:1464:U:O4	70:B2:1525:A:N6	2.36	0.59
70:B2:1758:A:H4'	81:AS:85:ASN:ND2	2.17	0.59
13:CT:75:ILE:HD12	13:CT:88:ARG:HE	1.68	0.59
48:AL:56:LYS:NZ	70:B2:332:U:OP2	2.32	0.59
55:AZ:46:GLN:O	55:AZ:77:LYS:NZ	2.36	0.59
55:AZ:48:LEU:HD23	55:AZ:50:ASP:HB2	1.83	0.59
60:Af:130:VAL:HG21	60:Af:142:GLY:H	1.66	0.59
69:A5:138:A:H2'	69:A5:139:U:H4'	1.85	0.59
74:AF:44:LYS:HG3	74:AF:51:CYS:HB2	1.84	0.59
45:AM:94:GLU:O	45:AM:106:LYS:NZ	2.36	0.59
66:AI:146:LYS:HE3	70:B2:186:A:H3'	1.85	0.59
2:CL:178:ALA:HB1	5:Ca:147:LEU:HD13	1.85	0.58
6:CN:44:ARG:NH2	6:CN:121:ILE:O	2.36	0.58
14:CP:8:SER:OG	14:CP:9:ASP:N	2.36	0.58
43:AO:102:GLY:O	43:AO:106:LYS:NZ	2.35	0.58
49:AR:92:GLU:HG3	49:AR:95:ILE:HB	1.85	0.58
69:A5:285:G:OP2	69:A5:336:A:N6	2.35	0.58
69:A5:318:G:H2'	69:A5:319:G:H8	1.68	0.58
70:B2:1758:A:C4'	81:AS:85:ASN:ND2	2.66	0.58
70:B2:1786:G:OP2	70:B2:1788:C:N4	2.36	0.58
16:CY:30:MET:HE1	16:CY:78:PHE:HA	1.85	0.58
17:CZ:46:ILE:HA	17:CZ:70:PRO:HA	1.85	0.58
37:CG:42:LYS:O	37:CG:49:ASN:ND2	2.36	0.58
70:B2:1317:U:O4	70:B2:1341:C:N4	2.36	0.58
2:CL:48:ARG:NH1	19:Ch:117:ARG:O	2.36	0.58
17:CZ:55:LYS:NZ	69:A5:3008:U:OP2	2.36	0.58
21:CB:332:MET:HE1	21:CB:368:ILE:HD13	1.85	0.58
36:CE:119:LEU:HD11	36:CE:165:ASP:HB2	1.85	0.58
52:AA:85:ARG:NH2	52:AA:201:LEU:O	2.36	0.58
55:AZ:47:VAL:CB	81:AS:55:ARG:CD	2.81	0.58
55:AZ:48:LEU:CG	81:AS:7:GLU:HB3	2.32	0.58
62:AE:35:PRO:HB3	62:AE:145:ARG:HH22	1.67	0.58
70:B2:1695:A:N7	81:AS:82:TRP:NE1	2.45	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:AF:76:PRO:HG2	74:AF:99:THR:HG21	1.85	0.58
18:Cr:105:LYS:O	18:Cr:108:LYS:NZ	2.36	0.58
21:CB:343:ARG:NH2	69:A5:3878:U:O3'	2.36	0.58
58:AD:105:GLU:HA	58:AD:108:ARG:HB2	1.85	0.58
62:AE:148:ARG:NH1	70:B2:124:U:OP1	2.37	0.58
69:A5:2071:A:H61	69:A5:2081:U:H3	1.50	0.58
68:Cz:174:MET:HB3	68:Cz:178:GLU:HB3	1.86	0.58
70:B2:1307:C:H2'	70:B2:1350:G:H22	1.68	0.58
79:Cg:3:GLN:O	79:Cg:3:GLN:HG3	2.00	0.58
10:CR:70:ARG:HE	10:CR:75:HIS:HB2	1.67	0.58
12:CS:165:LYS:NZ	25:Cf:44:TYR:O	2.35	0.58
35:CH:20:VAL:HG21	35:CH:45:MET:HB3	1.84	0.58
55:AZ:75:ARG:NH1	55:AZ:77:LYS:O	2.37	0.58
67:AQ:45:GLU:HA	67:AQ:47:LYS:HG2	1.85	0.58
67:AQ:56:PRO:HA	67:AQ:60:LEU:HD13	1.84	0.58
70:B2:1262:C:OP1	81:AS:139:THR:HG21	2.04	0.58
21:CB:301:ASN:N	21:CB:311:ASP:O	2.30	0.58
25:Cf:28:LYS:HD3	25:Cf:39:VAL:HA	1.84	0.58
58:AD:55:THR:O	58:AD:92:LYS:NZ	2.35	0.58
67:AQ:148:ARG:NH1	70:B2:1279:U:O2	2.36	0.58
70:B2:1808:G:H21	75:Ac:20:GLN:HG2	1.67	0.58
4:CM:17:ALA:HA	4:CM:21:LYS:HE2	1.85	0.58
20:Cb:4:SER:OG	20:Cb:5:LYS:N	2.34	0.58
46:Ad:15:GLY:O	46:Ad:19:ARG:NH1	2.37	0.58
49:AR:48:ASN:ND2	70:B2:1582:C:OP1	2.37	0.58
59:Ae:103:ARG:NH2	70:B2:480:A:OP2	2.37	0.58
61:AJ:115:VAL:HG21	61:AJ:130:LEU:HD11	1.85	0.58
64:AG:27:PHE:HA	64:AG:30:LYS:HE3	1.85	0.58
70:B2:1649:U:H1'	81:AS:135:HIS:CD2	2.35	0.58
3:CV:123:LYS:HB2	3:CV:140:ALA:HB2	1.86	0.58
6:CN:144:ARG:NH2	69:A5:130:C:OP1	2.37	0.58
37:CG:86:HIS:HB3	37:CG:89:SER:H	1.67	0.58
64:AG:57:ASP:O	64:AG:60:GLY:N	2.36	0.58
69:A5:426:A:N3	69:A5:805:C:O2'	2.35	0.58
74:AF:171:ARG:HA	74:AF:174:ASN:HB2	1.85	0.58
6:CN:201:HIS:HB2	6:CN:204:ARG:HB3	1.86	0.58
17:CZ:91:SER:O	17:CZ:94:LYS:NZ	2.37	0.58
37:CG:137:LYS:HD2	37:CG:138:PRO:HD2	1.86	0.58
41:Ag:114:PHE:HE2	41:Ag:118:ASN:HD22	1.52	0.58
69:A5:2651:G:N2	69:A5:2652:U:O4	2.33	0.58
70:B2:1220:A:H2'	70:B2:1221:A:H8	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:B2:1651:C:C4	81:AS:137:LYS:HA	2.39	0.58
74:AF:136:GLN:HA	74:AF:139:VAL:HG12	1.86	0.58
80:CD:39:ALA:HB3	80:CD:77:THR:HG21	1.84	0.58
6:CN:85:LYS:NZ	69:A5:296:C:OP1	2.36	0.57
6:CN:114:ARG:NH2	6:CN:153:LYS:O	2.37	0.57
9:CQ:40:ASN:ND2	69:A5:1183:U:O2	2.37	0.57
64:AG:179:ARG:HH21	70:B2:138:U:H2'	1.69	0.57
70:B2:985:A:H61	70:B2:1001:G:H5'	1.67	0.57
72:AT:63:HIS:HB3	72:AT:67:ARG:HB3	1.85	0.57
15:CX:260:ARG:NH1	69:A5:1893:C:OP1	2.37	0.57
40:A8:91:C:H5''	77:Cj:76:ASN:HD21	1.69	0.57
69:A5:1437:A:O2'	69:A5:1499:C:N4	2.37	0.57
8:CD:99:TYR:HE1	8:CD:164:LYS:HB3	1.69	0.57
9:CQ:99:THR:HG22	9:CQ:119:GLU:HB2	1.85	0.57
12:CS:163:ASN:O	25:Cf:43:LYS:NZ	2.37	0.57
30:Cm:119:ASN:N	30:Cm:119:ASN:OD1	2.38	0.57
49:AR:114:ILE:HG12	49:AR:115:ARG:HG2	1.86	0.57
55:AZ:48:LEU:HG	81:AS:7:GLU:CG	2.34	0.57
56:Aa:19:LYS:HD3	70:B2:963:G:H22	1.69	0.57
68:Cz:85:MET:HG2	68:Cz:87:ALA:H	1.68	0.57
69:A5:1280:C:H42	69:A5:1305:A:H61	1.52	0.57
69:A5:1984:U:H3	69:A5:2088:G:H1	1.51	0.57
69:A5:2825:A:N1	69:A5:2893:U:N3	2.51	0.57
16:CY:126:ARG:NH1	69:A5:203:A:OP2	2.38	0.57
22:CF:220:PRO:O	69:A5:1381:U:O2'	2.22	0.57
26:Ci:47:THR:OG1	26:Ci:51:ARG:NH1	2.36	0.57
42:AU:31:VAL:HG12	42:AU:32:ARG:HH21	1.69	0.57
51:AB:163:GLN:NE2	70:B2:1152:G:OP1	2.37	0.57
69:A5:3845:A:H8	69:A5:3847:U:H6	1.52	0.57
5:Ca:9:THR:HG23	5:Ca:10:ARG:HG2	1.86	0.57
6:CN:143:ARG:NH2	69:A5:141:U:O2	2.37	0.57
12:CS:157:ARG:NH2	69:A5:3755:A:OP1	2.38	0.57
37:CG:111:SER:HB3	37:CG:114:ALA:HB3	1.86	0.57
41:Ag:237:ILE:HA	41:Ag:253:TYR:HA	1.86	0.57
61:AJ:132:ARG:NH1	61:AJ:144:ASN:O	2.37	0.57
62:AE:30:ARG:NH2	70:B2:303:C:O2'	2.38	0.57
69:A5:3588:G:H2'	69:A5:3589:G:H8	1.69	0.57
4:CM:117:ARG:HH22	69:A5:3767:G:H3'	1.70	0.57
32:Cp:52:VAL:HG21	69:A5:2106:C:H4'	1.85	0.57
36:CE:85:SER:O	69:A5:754:A:O2'	2.23	0.57
36:CE:167:TYR:OH	36:CE:201:ASP:OD2	2.22	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:CG:44:PHE:O	37:CG:51:GLN:NE2	2.38	0.57
43:AO:61:LYS:HG3	43:AO:77:ALA:HB2	1.86	0.57
52:AA:134:ILE:HG23	52:AA:144:VAL:HG21	1.86	0.57
58:AD:47:ARG:HA	58:AD:85:ARG:HG2	1.86	0.57
65:AH:156:LEU:HD11	65:AH:164:ILE:HG21	1.86	0.57
69:A5:2200:A:P	80:Cd:41:ARG:NH2	2.78	0.57
4:CM:5:ARG:HB2	12:CS:154:LEU:HB2	1.86	0.57
22:CF:188:ILE:HG23	22:CF:193:ASP:HB3	1.87	0.57
24:Ce:6:ALA:HB2	24:Ce:92:ARG:HD2	1.85	0.57
54:AY:40:GLU:O	54:AY:44:LYS:NZ	2.36	0.57
56:Aa:98:PRO:HB2	56:Aa:100:ARG:HB2	1.87	0.57
60:Af:108:VAL:HG13	60:Af:114:ILE:HG13	1.87	0.57
67:AQ:15:PHE:H	67:AQ:92:LYS:HD3	1.70	0.57
69:A5:2469:U:H3'	69:A5:2470:U:H2'	1.87	0.57
70:B2:1758:A:C5'	81:AS:37:GLY:H	2.18	0.57
70:B2:1805:U:OP2	74:AF:89:LYS:NZ	2.34	0.57
10:CR:103:ARG:NH1	69:A5:2035:C:OP2	2.36	0.57
55:AZ:49:PHE:CA	81:AS:7:GLU:HB2	2.32	0.57
69:A5:474:A:N6	69:A5:524:A:OP1	2.35	0.57
69:A5:476:U:O2'	69:A5:518:G:N7	2.31	0.57
69:A5:928:U:O2	69:A5:973:G:N2	2.38	0.57
69:A5:3347:G:N2	69:A5:3350:U:O2	2.36	0.57
69:A5:3593:A:OP1	80:Cd:38:ARG:NH1	2.35	0.57
70:B2:843:G:O2'	70:B2:873:A:N6	2.37	0.57
4:CM:146:ASP:O	4:CM:150:ARG:NH1	2.38	0.57
15:CX:191:ARG:NH1	40:A8:59:G:OP1	2.38	0.57
24:Ce:84:LEU:HD21	24:Ce:114:ALA:HB2	1.87	0.57
32:Cp:59:ARG:NH1	69:A5:2039:G:OP1	2.35	0.57
41:Ag:245:ASN:ND2	41:Ag:296:GLY:O	2.37	0.57
52:AA:181:GLU:HA	52:AA:184:ARG:HB2	1.85	0.57
70:B2:1832:C:O2'	70:B2:1957:A:N1	2.37	0.57
8:CD:187:THR:OG1	8:CD:188:LYS:N	2.38	0.57
29:CC:308:PRO:HB2	29:CC:310:LYS:HD3	1.86	0.57
36:CE:78:ARG:NH2	69:A5:460:A:OP1	2.38	0.57
45:AM:90:LYS:HE2	45:AM:112:GLY:HA2	1.87	0.57
55:AZ:46:GLN:CG	81:AS:23:LYS:HA	2.34	0.57
55:AZ:50:ASP:C	81:AS:8:LYS:HZ2	2.13	0.57
57:Ab:30:SER:OG	57:Ab:31:TYR:N	2.36	0.57
68:Cz:67:ILE:HG21	68:Cz:147:LYS:HE2	1.87	0.57
69:A5:167:A:H61	69:A5:280:C:H42	1.51	0.57
69:A5:1990:G:OP2	76:CU:255:LYS:NZ	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Cf:68:GLU:OE1	69:A5:782:G:N2	2.38	0.56
36:CE:71:THR:O	36:CE:73:THR:OG1	2.21	0.56
50:AP:20:TYR:CE1	81:AS:90:ILE:CG2	2.88	0.56
50:AP:109:GLU:N	81:AS:118:ARG:NH2	2.53	0.56
54:AY:103:GLN:HG2	54:AY:105:ARG:HH21	1.69	0.56
55:AZ:51:LYS:H	81:AS:6:PRO:HA	1.69	0.56
65:AH:8:ILE:HG22	65:AH:44:ILE:HG12	1.86	0.56
69:A5:1551:U:H2'	69:A5:1552:A:H8	1.70	0.56
2:CL:46:PHE:HB3	2:CL:48:ARG:HG3	1.87	0.56
11:CA:124:GLY:O	11:CA:128:ARG:NH1	2.38	0.56
21:CB:45:CYS:SG	21:CB:348:ARG:NH1	2.78	0.56
23:Cc:78:ASN:ND2	69:A5:2042:A:N7	2.52	0.56
37:CG:78:ARG:HG3	69:A5:2908:U:H5'	1.88	0.56
44:AX:54:LYS:HD2	44:AX:91:LEU:HD23	1.86	0.56
62:AE:36:HIS:CE1	62:AE:88:ASP:OD2	2.58	0.56
67:AQ:17:ARG:HH22	67:AQ:20:THR:HA	1.70	0.56
69:A5:757:A:O2'	69:A5:3843:U:OP1	2.23	0.56
69:A5:2827:G:N7	69:A5:2888:A:N6	2.53	0.56
70:B2:1290:A:N6	70:B2:1649:U:O5'	2.39	0.56
9:CQ:146:ARG:NH2	69:A5:820:A:OP1	2.38	0.56
10:CR:122:ASP:OD2	10:CR:126:LYS:NZ	2.39	0.56
11:CA:94:ALA:HB3	11:CA:102:MET:HB3	1.87	0.56
15:CX:258:TYR:OH	69:A5:1765:U:OP1	2.24	0.56
19:Ch:85:LYS:HD3	19:Ch:87:LYS:HE3	1.85	0.56
24:Ce:92:ARG:HG3	24:Ce:93:VAL:HG13	1.87	0.56
24:Ce:128:LEU:HD13	24:Ce:130:SER:HB2	1.86	0.56
37:CG:110:GLU:O	37:CG:200:ARG:NE	2.37	0.56
51:AB:119:LYS:HD3	70:B2:1019:U:H5''	1.85	0.56
56:Aa:34:LYS:NZ	70:B2:1990:U:O4	2.38	0.56
58:AD:99:CYS:SG	58:AD:100:ALA:N	2.77	0.56
63:AC:173:SER:HB3	70:B2:1173:A:H5'	1.88	0.56
64:AG:137:ARG:NH2	70:B2:140:G:N7	2.52	0.56
65:AH:101:LYS:NZ	65:AH:102:PRO:O	2.39	0.56
69:A5:462:C:OP1	69:A5:540:G:N2	2.39	0.56
69:A5:935:A:N6	69:A5:966:U:O4	2.38	0.56
70:B2:249:U:H3'	70:B2:250:U:H4'	1.87	0.56
70:B2:1068:U:H3	70:B2:1107:A:H61	1.52	0.56
70:B2:1758:A:C5'	81:AS:37:GLY:N	2.69	0.56
74:AF:54:ILE:HG23	74:AF:136:GLN:HG3	1.87	0.56
24:Ce:15:ARG:NH2	24:Ce:18:HIS:O	2.38	0.56
29:CC:172:ILE:HG12	29:CC:175:ARG:HH21	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:CE:119:LEU:HD23	36:CE:123:LEU:HD23	1.87	0.56
41:Ag:152:VAL:HA	41:Ag:170:GLY:HA2	1.87	0.56
65:AH:71:GLN:HA	65:AH:74:GLN:HB2	1.85	0.56
69:A5:840:U:O2	69:A5:842:A:N6	2.38	0.56
69:A5:1282:U:H3	69:A5:1303:C:H42	1.52	0.56
2:CL:120:ARG:NH1	2:CL:135:ALA:O	2.36	0.56
10:CR:192:ASP:HA	10:CR:195:ALA:HB3	1.88	0.56
14:CP:182:MET:SD	69:A5:3777:U:O2'	2.64	0.56
34:CJ:73:ILE:HD11	69:A5:3213:C:H5'	1.88	0.56
36:CE:119:LEU:HD13	36:CE:139:ARG:HH12	1.70	0.56
50:AP:21:ARG:HD2	81:AS:93:GLY:HA2	1.82	0.56
55:AZ:48:LEU:CA	81:AS:7:GLU:HG3	2.15	0.56
60:Af:80:ARG:NH2	70:B2:1297:C:OP1	2.38	0.56
68:Cz:88:GLU:OE2	68:Cz:118:LYS:NZ	2.38	0.56
77:Cj:18:LEU:HA	77:Cj:25:SER:HA	1.86	0.56
80:Cd:85:LEU:HD23	80:Cd:103:VAL:HG13	1.88	0.56
10:CR:37:SER:OG	10:CR:38:ARG:N	2.39	0.56
14:CP:43:ARG:NH2	69:A5:3966:U:OP1	2.39	0.56
24:Ce:127:ARG:NH1	69:A5:1633:G:OP1	2.38	0.56
51:AB:34:LYS:HE3	51:AB:42:ARG:HD2	1.88	0.56
69:A5:1260:A:N3	69:A5:3165:U:O2'	2.39	0.56
69:A5:2819:A:H3'	69:A5:2820:G:H5''	1.88	0.56
12:CS:51:LEU:HD13	13:CT:152:PRO:HB3	1.88	0.56
50:AP:45:ARG:NH1	70:B2:1742:A:OP2	2.39	0.56
52:AA:27:SER:O	52:AA:47:ASN:ND2	2.38	0.56
69:A5:1293:A:H2'	69:A5:1294:U:H5''	1.87	0.56
70:B2:1636:A:H4'	70:B2:1637:G:H3'	1.88	0.56
79:Cg:19:LYS:HB3	79:Cg:35:VAL:HB	1.87	0.56
8:CD:107:ARG:NH1	8:CD:120:ALA:O	2.39	0.56
11:CA:152:SER:OG	69:A5:2536:G:N7	2.33	0.56
12:CS:83:ARG:HG2	12:CS:127:ILE:HD11	1.87	0.56
27:Ck:37:ARG:HD2	27:Ck:42:LEU:HD13	1.88	0.56
29:CC:116:ARG:NH1	69:A5:991:A:OP1	2.38	0.56
41:Ag:248:TRP:HB3	41:Ag:259:ILE:HD11	1.87	0.56
45:AM:111:CYS:SG	70:B2:1314:G:N2	2.79	0.56
54:AY:42:ARG:NH1	54:AY:53:PRO:O	2.39	0.56
68:Cz:36:ILE:HG22	68:Cz:165:LEU:HD22	1.88	0.56
70:B2:1271:A:N3	70:B2:1298:C:O2'	2.38	0.56
70:B2:1673:U:OP2	72:AT:11:GLN:NE2	2.38	0.56
24:Ce:7:TYR:HD2	36:CE:79:PRO:HA	1.71	0.56
44:AX:68:LYS:NZ	70:B2:575:A:OP1	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:AZ:51:LYS:H	81:AS:8:LYS:HZ3	1.51	0.56
57:Ab:11:LEU:HD23	57:Ab:13:ALA:H	1.71	0.56
64:AG:51:ARG:NH2	70:B2:1875:G:OP2	2.39	0.56
69:A5:542:C:H42	69:A5:760:G:H1	1.54	0.56
76:CU:285:TYR:OH	76:CU:287:ARG:NH2	2.39	0.56
14:CP:93:GLN:OE1	69:A5:403:A:N6	2.38	0.56
30:Cm:78:ILE:O	30:Cm:83:ARG:NH2	2.39	0.56
36:CE:115:LEU:HD21	36:CE:124:LEU:HB3	1.88	0.56
56:Aa:7:ASN:OD1	70:B2:1021:A:N6	2.35	0.56
56:Aa:10:ARG:HE	56:Aa:95:ARG:HH22	1.52	0.56
69:A5:2177:G:O2'	69:A5:3601:U:OP1	2.23	0.56
70:B2:631:C:O2	70:B2:1193:C:O2'	2.22	0.56
1:CO:67:ASN:HB3	1:CO:70:ARG:HG3	1.88	0.55
8:CD:15:ARG:NH1	69:A5:3221:A:OP2	2.38	0.55
10:CR:176:ARG:NH1	70:B2:939:G:OP2	2.39	0.55
11:CA:36:GLU:HA	11:CA:91:GLY:HA2	1.88	0.55
12:CS:139:ARG:NE	69:A5:1428:G:OP1	2.38	0.55
26:CI:27:GLY:HA3	26:CI:41:ASN:HD21	1.70	0.55
54:AY:119:ARG:HH22	70:B2:85:A:H5''	1.71	0.55
70:B2:1305:A:N6	70:B2:1354:G:O2'	2.40	0.55
3:CV:48:ARG:NH1	3:CV:49:LEU:O	2.39	0.55
5:Ca:27:ARG:NH1	69:A5:1138:C:OP2	2.39	0.55
7:CI:44:GLU:OE1	7:CI:185:ARG:NH1	2.39	0.55
21:CB:26:ARG:NH1	21:CB:180:VAL:O	2.40	0.55
37:CG:116:LYS:NZ	69:A5:148:U:O4	2.39	0.55
49:AR:109:LEU:HD11	52:AA:52:GLY:HA3	1.88	0.55
67:AQ:8:PRO:HG2	67:AQ:28:LYS:HD3	1.87	0.55
70:B2:491:G:N2	70:B2:510:U:O2	2.40	0.55
70:B2:1261:C:C5'	81:AS:130:ARG:HD3	2.35	0.55
12:CS:171:LYS:HG2	12:CS:173:ARG:HG2	1.88	0.55
14:CP:27:LYS:NZ	69:A5:1688:A:OP2	2.27	0.55
28:CI:2:ALA:N	69:A5:1736:G:O6	2.39	0.55
35:CH:9:CYS:SG	35:CH:52:THR:OG1	2.62	0.55
62:AE:1:MET:O	70:B2:403:G:O2'	2.23	0.55
65:AH:142:ILE:HA	65:AH:152:VAL:HA	1.88	0.55
1:CO:170:LEU:O	1:CO:174:ARG:NH1	2.40	0.55
2:CL:59:ARG:NH1	2:CL:66:HIS:O	2.39	0.55
12:CS:8:LYS:NZ	12:CS:35:PRO:O	2.40	0.55
13:CT:124:GLN:HE21	13:CT:125:TRP:HE3	1.54	0.55
32:Cp:4:ARG:NH2	69:A5:1038:G:O6	2.39	0.55
37:CG:151:LEU:HB3	37:CG:157:ALA:HB2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:AY:37:ASN:HD22	70:B2:529:C:H5''	1.70	0.55
58:AD:44:THR:OG1	58:AD:47:ARG:NH1	2.39	0.55
69:A5:2827:G:O6	69:A5:2889:C:N4	2.40	0.55
70:B2:1695:A:C1'	81:AS:83:PHE:CZ	2.79	0.55
1:CO:116:LYS:O	69:A5:3720:A:N6	2.29	0.55
17:CZ:38:PHE:HB3	69:A5:2024:U:H5''	1.89	0.55
43:AO:96:LYS:HE3	43:AO:132:VAL:HG21	1.88	0.55
48:AL:122:ILE:HB	48:AL:143:SER:HB3	1.89	0.55
69:A5:1912:G:OP1	69:A5:1923:A:N6	2.39	0.55
69:A5:3592:C:O4'	69:A5:3621:A:N6	2.40	0.55
70:B2:136:A:N6	70:B2:139:U:O2'	2.40	0.55
2:CL:80:LEU:HB3	2:CL:85:ILE:HG22	1.89	0.55
15:CX:189:ARG:HH22	40:A8:95:A:H5''	1.72	0.55
21:CB:18:PRO:O	21:CB:20:LYS:N	2.39	0.55
29:CC:118:VAL:O	29:CC:123:ARG:NH2	2.40	0.55
50:AP:21:ARG:HD3	81:AS:90:ILE:HA	1.88	0.55
54:AY:110:GLU:OE2	54:AY:111:ARG:NH2	2.40	0.55
58:AD:17:GLY:O	58:AD:20:LYS:NZ	2.37	0.55
67:AQ:19:LYS:NZ	70:B2:1802:G:O6	2.39	0.55
69:A5:1369:C:O2'	69:A5:1412:A:N1	2.37	0.55
69:A5:2850:A:N6	69:A5:2866:G:O6	2.40	0.55
70:B2:369:G:O2'	70:B2:878:C:N4	2.36	0.55
73:AK:43:VAL:HA	73:AK:47:MET:HB3	1.89	0.55
74:AF:143:VAL:O	74:AF:148:ARG:NH1	2.39	0.55
1:CO:195:ASN:O	1:CO:199:LYS:NZ	2.35	0.55
2:CL:138:SER:HB3	2:CL:141:GLU:HB2	1.87	0.55
4:CM:130:LEU:HD21	4:CM:132:LYS:HD2	1.88	0.55
18:Cr:95:LYS:HD3	36:CE:67:ALA:HB1	1.88	0.55
21:CB:54:THR:OG1	21:CB:369:ASP:O	2.25	0.55
25:Cf:101:LYS:HE3	25:Cf:111:LYS:HA	1.89	0.55
36:CE:46:ARG:O	69:A5:740:G:N2	2.38	0.55
63:AC:89:VAL:HG12	63:AC:111:VAL:HG12	1.87	0.55
69:A5:1084:A:OP1	77:Cj:5:THR:OG1	2.16	0.55
69:A5:1582:U:H2'	69:A5:1583:G:H8	1.71	0.55
70:B2:623:G:N2	70:B2:1194:C:O2	2.32	0.55
70:B2:646:U:OP2	71:AW:32:LYS:NZ	2.39	0.55
74:AF:214:TYR:O	74:AF:218:LYS:NZ	2.39	0.55
16:CY:54:GLU:HB2	16:CY:108:LYS:HB3	1.89	0.55
21:CB:1:MET:SD	21:CB:2:SER:N	2.80	0.55
25:Cf:110:ARG:HE	25:Cf:113:ARG:H	1.53	0.55
34:CJ:103:ASN:ND2	34:CJ:111:GLY:O	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:A7:21:G:H1	39:A7:56:G:H1	1.55	0.55
41:Ag:7:LEU:HD11	41:Ag:309:ARG:HB2	1.87	0.55
42:AU:101:LYS:O	42:AU:104:THR:OG1	2.24	0.55
45:AM:26:GLN:HA	45:AM:29:LEU:HB2	1.89	0.55
50:AP:37:VAL:HB	50:AP:45:ARG:HG2	1.87	0.55
66:AI:192:LEU:HD23	66:AI:197:LEU:HA	1.89	0.55
11:CA:196:TRP:HE3	11:CA:197:PRO:HD2	1.71	0.55
13:CT:40:VAL:HG11	13:CT:64:ILE:HG13	1.87	0.55
22:CF:221:THR:H	22:CF:250:LYS:HB3	1.71	0.55
25:Cf:79:ARG:HG2	25:Cf:128:THR:HB	1.87	0.55
31:Cn:14:LYS:O	31:Cn:18:ARG:NE	2.35	0.55
50:AP:47:ARG:NH2	70:B2:1747:A:O2'	2.40	0.55
55:AZ:51:LYS:HE3	81:AS:6:PRO:HG3	0.66	0.55
58:AD:145:ARG:O	70:B2:587:A:N6	2.40	0.55
64:AG:59:GLN:OE1	64:AG:72:ARG:NH2	2.40	0.55
64:AG:92:ARG:NH2	70:B2:398:C:O2'	2.40	0.55
70:B2:127:U:H3	70:B2:180:A:H61	1.55	0.55
70:B2:487:U:H2'	70:B2:488:A:H8	1.72	0.55
6:CN:3:ALA:H	37:CG:146:ASN:HA	1.72	0.55
11:CA:68:ARG:NH1	69:A5:1863:U:OP1	2.40	0.55
67:AQ:132:LYS:HA	67:AQ:139:ALA:HA	1.89	0.55
69:A5:2266:U:H3	69:A5:2475:A:H61	1.55	0.55
70:B2:1661:A:H3'	74:AF:107:ARG:HH22	1.72	0.55
70:B2:1777:U:H2'	70:B2:1778:A:H8	1.72	0.55
72:AT:64:LEU:HD13	72:AT:69:PRO:HA	1.89	0.55
74:AF:147:PRO:HB3	74:AF:222:LEU:HD21	1.89	0.55
1:CO:91:PRO:HD3	69:A5:1389:C:H4'	1.89	0.54
18:Cr:5:SER:OG	18:Cr:42:TYR:OH	2.23	0.54
51:AB:184:LEU:HA	51:AB:187:LEU:HB3	1.89	0.54
69:A5:2277:G:N1	69:A5:2459:C:N3	2.55	0.54
69:A5:2986:G:H2'	69:A5:2987:A:H8	1.73	0.54
69:A5:3909:A:N7	69:A5:3944:A:O2'	2.31	0.54
70:B2:1321:A:N6	70:B2:1332:G:O2'	2.40	0.54
70:B2:1758:A:P	81:AS:37:GLY:H	2.29	0.54
5:Ca:4:ILE:HG23	5:Ca:7:LYS:HD2	1.90	0.54
5:Ca:33:ARG:NH1	69:A5:999:U:OP1	2.40	0.54
11:CA:206:PRO:HD3	11:CA:213:GLY:HA2	1.89	0.54
18:Cr:43:ARG:HG2	18:Cr:48:VAL:HG22	1.89	0.54
41:Ag:35:SER:OG	41:Ag:36:ARG:N	2.39	0.54
44:AX:119:ARG:NH2	70:B2:1223:U:OP2	2.39	0.54
64:AG:60:GLY:O	70:B2:151:G:N2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:AG:96:SER:OG	70:B2:425:A:OP1	2.24	0.54
68:Cz:25:LYS:NZ	69:A5:2850:A:OP1	2.40	0.54
69:A5:3950:A:O5'	80:Cd:28:LYS:HD2	2.08	0.54
1:CO:29:LEU:O	1:CO:103:ARG:NH1	2.39	0.54
4:CM:52:LEU:HD22	12:CS:154:LEU:HD11	1.90	0.54
30:Cm:109:ASN:ND2	30:Cm:117:HIS:O	2.40	0.54
69:A5:2591:A:H2'	69:A5:2592:A:C8	2.42	0.54
70:B2:1080:A:OP1	70:B2:1972:G:N2	2.39	0.54
70:B2:1437:A:N6	70:B2:1568:G:O2'	2.40	0.54
74:AF:142:ILE:HA	74:AF:145:SER:HB2	1.88	0.54
21:CB:174:ARG:NH1	69:A5:3895:A:OP1	2.39	0.54
38:A9:30:A:N7	69:A5:1:U:O2'	2.40	0.54
50:AP:86:MET:HB3	50:AP:119:LEU:HD23	1.89	0.54
57:Ab:14:GLU:OE2	57:Ab:18:LYS:NZ	2.40	0.54
79:Cg:54:ILE:HG23	79:Cg:70:LYS:HA	1.89	0.54
7:CI:19:LYS:NZ	7:CI:95:HIS:O	2.40	0.54
21:CB:374:MET:O	69:A5:3904:G:O2'	2.25	0.54
34:CJ:17:MET:HB3	34:CJ:18:ARG:HH11	1.72	0.54
41:Ag:47:ARG:NH2	41:Ag:53:TYR:OH	2.35	0.54
55:AZ:61:VAL:O	55:AZ:110:ARG:NH1	2.40	0.54
60:Af:95:ARG:NH2	70:B2:1332:G:O2'	2.41	0.54
69:A5:2065:A:H3'	69:A5:2066:G:H8	1.73	0.54
70:B2:1553:A:H1'	70:B2:1559:A:H61	1.73	0.54
30:Cm:125:LYS:HG3	69:A5:3429:A:H5'	1.89	0.54
45:AM:95:TRP:NE1	45:AM:104:GLU:OE2	2.41	0.54
58:AD:179:LEU:HD22	58:AD:184:LEU:HD13	1.89	0.54
68:Cz:146:GLY:O	68:Cz:150:GLU:N	2.38	0.54
69:A5:589:A:N6	69:A5:618:U:O4	2.40	0.54
70:B2:44:U:OP2	70:B2:442:A:N6	2.36	0.54
70:B2:498:U:O2'	70:B2:502:C:N3	2.39	0.54
70:B2:1707:A:O2'	70:B2:1710:C:N4	2.40	0.54
4:CM:12:ILE:HG13	4:CM:82:LEU:HD11	1.90	0.54
5:Ca:117:HIS:ND1	69:A5:984:U:O4	2.40	0.54
8:CD:52:ILE:HG13	8:CD:147:ASP:HB3	1.90	0.54
9:CQ:39:THR:O	9:CQ:39:THR:OG1	2.24	0.54
18:Cr:80:ASN:OD1	18:Cr:84:VAL:N	2.40	0.54
21:CB:229:LYS:HG3	21:CB:272:LYS:HD3	1.89	0.54
34:CJ:153:SER:OG	34:CJ:154:GLY:N	2.40	0.54
36:CE:194:PRO:HD3	69:A5:3839:A:H61	1.72	0.54
54:AY:17:ARG:O	62:AE:94:LYS:NZ	2.40	0.54
55:AZ:64:TYR:O	55:AZ:110:ARG:NH1	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:A5:412:U:O2'	69:A5:414:A:N7	2.38	0.54
69:A5:2771:G:O2'	69:A5:3513:A:N6	2.40	0.54
70:B2:330:G:H1	70:B2:348:C:H42	1.55	0.54
70:B2:1304:G:N1	70:B2:1635:U:O2'	2.41	0.54
70:B2:1670:G:OP2	72:AT:43:LYS:NZ	2.41	0.54
70:B2:1847:A:N6	70:B2:1940:G:O2'	2.40	0.54
72:AT:11:GLN:HA	72:AT:14:VAL:HG22	1.88	0.54
81:AS:13:LEU:O	81:AS:19:ASN:ND2	2.41	0.54
10:CR:61:TYR:HB2	69:A5:2001:U:H5''	1.89	0.54
34:CJ:38:LEU:O	34:CJ:42:ALA:N	2.40	0.54
35:CH:103:THR:HG21	35:CH:132:VAL:HG13	1.90	0.54
39:A7:67:G:H22	39:A7:108:G:H1	1.55	0.54
45:AM:33:LEU:HG	45:AM:97:GLY:HA2	1.89	0.54
69:A5:2487:C:H1'	69:A5:3918:A:H8	1.71	0.54
69:A5:3688:A:O2'	69:A5:3691:A:N1	2.35	0.54
70:B2:225:G:O2'	70:B2:236:A:N6	2.41	0.54
81:AS:42:ASN:O	81:AS:46:LYS:NZ	2.40	0.54
8:CD:86:TYR:OH	8:CD:250:ASP:O	2.26	0.54
8:CD:100:CYS:O	8:CD:104:LEU:N	2.39	0.54
9:CQ:65:ARG:HD3	69:A5:872:A:C5	2.43	0.54
10:CR:172:ARG:HH22	70:B2:938:G:H2'	1.72	0.54
23:Cc:21:VAL:HG11	23:Cc:96:ILE:HG12	1.89	0.54
24:Cc:82:ARG:NH2	69:A5:1627:U:OP1	2.41	0.54
35:CH:5:ASN:ND2	35:CH:56:GLU:OE2	2.41	0.54
44:AX:5:ARG:N	70:B2:1191:C:OP2	2.38	0.54
50:AP:19:THR:O	81:AS:91:ILE:HG23	2.07	0.54
50:AP:45:ARG:NH2	70:B2:1741:A:OP1	2.41	0.54
55:AZ:46:GLN:C	81:AS:23:LYS:CG	2.79	0.54
66:AI:118:VAL:HB	66:AI:139:LEU:HD13	1.90	0.54
69:A5:889:G:O6	69:A5:898:A:N6	2.41	0.54
69:A5:1375:G:OP2	69:A5:1606:G:O2'	2.17	0.54
4:CM:5:ARG:HB3	4:CM:57:LEU:HB2	1.90	0.54
8:CD:10:LYS:NZ	39:A7:66:G:OP1	2.41	0.54
21:CB:229:LYS:H	21:CB:234:ARG:NH2	2.06	0.54
29:CC:200:ARG:NH1	69:A5:358:C:OP2	2.40	0.54
36:CE:57:LYS:NZ	36:CE:65:SER:OG	2.37	0.54
45:AM:59:LEU:HD22	45:AM:115:VAL:HA	1.89	0.54
50:AP:21:ARG:CD	81:AS:90:ILE:O	2.56	0.54
50:AP:50:ARG:HE	70:B2:1746:A:H5''	1.73	0.54
50:AP:109:GLU:H	81:AS:118:ARG:NH2	2.05	0.54
58:AD:73:ALA:HB1	73:AK:19:GLY:HA3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:A5:1236:C:OP2	69:A5:1237:G:N2	2.41	0.54
5:Ca:62:PHE:O	69:A5:322:G:O2'	2.27	0.53
6:CN:75:VAL:HG11	6:CN:80:THR:HG22	1.90	0.53
10:CR:105:LEU:HD23	10:CR:138:LEU:HD23	1.89	0.53
41:Ag:100:ARG:HH11	41:Ag:136:LEU:HD13	1.73	0.53
48:AL:23:PRO:HD2	70:B2:211:U:H4'	1.89	0.53
48:AL:123:VAL:HG22	48:AL:142:VAL:HG12	1.88	0.53
64:AG:10:THR:HA	64:AG:128:THR:HG23	1.90	0.53
70:B2:393:G:H2'	70:B2:394:G:H8	1.72	0.53
70:B2:1205:U:H2'	70:B2:1206:G:H8	1.71	0.53
70:B2:1261:C:H5''	81:AS:130:ARG:HD3	1.89	0.53
70:B2:1383:A:N3	70:B2:1384:G:N2	2.55	0.53
73:AK:87:ILE:HG22	73:AK:88:VAL:HG12	1.90	0.53
74:AF:68:LYS:HA	74:AF:71:PHE:HB3	1.89	0.53
5:Ca:132:LYS:NZ	5:Ca:136:ASP:OD2	2.38	0.53
12:CS:46:TYR:OH	39:A7:94:C:OP1	2.22	0.53
36:CE:116:LEU:HD21	36:CE:209:LEU:HD11	1.91	0.53
47:AN:87:ASP:OD1	47:AN:87:ASP:N	2.41	0.53
54:AY:121:THR:HB	54:AY:123:LYS:HE3	1.91	0.53
61:AJ:173:ARG:NH2	70:B2:544:C:OP2	2.37	0.53
62:AE:19:MET:HE2	62:AE:51:ARG:HH21	1.73	0.53
69:A5:1420:A:H2'	69:A5:1421:G:H8	1.71	0.53
69:A5:3950:A:O4'	80:Cd:28:LYS:HG3	2.08	0.53
70:B2:484:C:O2	70:B2:518:G:N2	2.41	0.53
70:B2:1427:U:O2'	70:B2:1428:A:N7	2.38	0.53
72:AT:59:SER:O	72:AT:63:HIS:ND1	2.41	0.53
74:AF:148:ARG:O	74:AF:172:ARG:NE	2.40	0.53
39:A7:87:G:N2	39:A7:90:A:OP2	2.39	0.53
44:AX:8:ARG:HG3	48:AL:99:PHE:HB2	1.91	0.53
62:AE:103:TYR:HA	62:AE:109:PHE:HA	1.90	0.53
69:A5:929:A:N7	69:A5:930:U:O2'	2.41	0.53
69:A5:2915:U:O2'	69:A5:2918:A:OP1	2.27	0.53
69:A5:3105:A:O2'	69:A5:3106:G:O4'	2.24	0.53
69:A5:3359:U:O4	69:A5:3391:U:O2'	2.19	0.53
45:AM:42:ILE:O	45:AM:46:CYS:N	2.41	0.53
52:AA:163:CYS:SG	52:AA:164:ASN:N	2.80	0.53
64:AG:159:ARG:HB3	64:AG:172:SER:HB3	1.91	0.53
70:B2:1736:U:O5'	81:AS:131:VAL:HG22	2.08	0.53
74:AF:165:VAL:HG11	75:Ac:40:ARG:HD2	1.89	0.53
8:CD:34:LYS:HA	13:CT:27:LEU:HD11	1.89	0.53
10:CR:42:ARG:NH2	69:A5:1885:U:OP1	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CA:2:GLY:HA2	11:CA:207:VAL:HG23	1.91	0.53
14:CP:77:LYS:HB3	69:A5:3525:A:H4'	1.90	0.53
21:CB:247:GLY:HA2	69:A5:2205:G:H5'	1.90	0.53
23:Cc:78:ASN:HB3	23:Cc:90:ARG:HB3	1.91	0.53
41:Ag:22:ALA:HB3	41:Ag:32:ILE:HB	1.91	0.53
44:AX:6:GLY:HA3	70:B2:641:U:H5'	1.90	0.53
45:AM:79:HIS:HD2	45:AM:80:GLN:HG3	1.73	0.53
48:AL:133:LYS:HG3	48:AL:134:THR:HG23	1.89	0.53
52:AA:209:GLU:HG3	70:B2:1592:C:H41	1.73	0.53
57:Ab:33:MET:HB2	57:Ab:46:VAL:HG22	1.91	0.53
64:AG:102:VAL:HG13	64:AG:106:MET:HG3	1.89	0.53
70:B2:1540:G:H21	72:AT:129:ARG:HH12	1.56	0.53
1:CO:4:LEU:O	25:Cf:53:LYS:NZ	2.42	0.53
6:CN:118:SER:HB3	6:CN:132:VAL:HG22	1.91	0.53
25:Cf:87:TYR:OH	36:CE:239:HIS:ND1	2.31	0.53
25:Cf:112:THR:O	25:Cf:115:ARG:NH2	2.27	0.53
36:CE:228:ASN:OD1	69:A5:3774:U:O2'	2.24	0.53
57:Ab:73:LEU:HD13	57:Ab:77:CYS:HB2	1.91	0.53
60:Af:99:LYS:HD2	60:Af:100:LEU:HB2	1.91	0.53
2:CL:110:GLN:O	2:CL:114:GLN:NE2	2.42	0.53
6:CN:183:THR:O	6:CN:183:THR:OG1	2.19	0.53
9:CQ:163:THR:O	9:CQ:163:THR:OG1	2.20	0.53
21:CB:40:PRO:O	21:CB:42:HIS:N	2.42	0.53
27:Ck:69:VAL:HG21	69:A5:2063:A:H1'	1.91	0.53
30:Cm:125:LYS:O	35:CH:171:ARG:NH1	2.42	0.53
61:AJ:134:ARG:HG2	61:AJ:144:ASN:HD21	1.73	0.53
62:AE:146:THR:HG21	70:B2:122:G:H21	1.74	0.53
65:AH:169:ASP:N	65:AH:169:ASP:OD1	2.41	0.53
66:AI:125:ARG:NH2	69:A5:3925:G:O3'	2.42	0.53
66:AI:126:ASN:HA	66:AI:129:HIS:HB2	1.91	0.53
70:B2:69:A:H61	70:B2:81:U:H3	1.56	0.53
6:CN:38:ARG:NH1	38:A9:16:U:OP1	2.41	0.53
6:CN:187:SER:HB3	6:CN:190:ALA:H	1.74	0.53
8:CD:33:ARG:NH2	39:A7:7:G:O3'	2.41	0.53
21:CB:110:LEU:O	21:CB:115:ARG:NH1	2.41	0.53
28:Cl:10:LYS:HD2	69:A5:2149:G:H5''	1.91	0.53
51:AB:32:ASP:HA	51:AB:46:LYS:HA	1.90	0.53
57:Ab:80:ARG:HB3	57:Ab:82:LYS:HZ1	1.74	0.53
62:AE:107:GLY:HA2	62:AE:189:LEU:HB3	1.90	0.53
62:AE:151:ASP:OD2	64:AG:217:ARG:NH2	2.41	0.53
62:AE:256:LEU:HD11	70:B2:845:G:H4'	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:B2:1736:U:O2'	81:AS:131:VAL:HG13	2.03	0.53
7:CI:101:LYS:HE2	7:CI:103:LEU:HG	1.90	0.53
8:CD:164:LYS:HA	8:CD:167:VAL:HG12	1.90	0.53
11:CA:14:SER:OG	69:A5:1111:C:OP1	2.27	0.53
11:CA:202:VAL:HG22	11:CA:217:GLN:HG3	1.89	0.53
16:CY:74:TYR:OH	40:A8:74:G:OP2	2.26	0.53
24:Ce:103:SER:HB3	69:A5:1630:G:H5''	1.89	0.53
29:CC:72:THR:HB	69:A5:2780:A:H5''	1.89	0.53
47:AN:124:ARG:NH2	70:B2:1054:A:OP2	2.42	0.53
55:AZ:46:GLN:HG2	81:AS:23:LYS:CA	2.37	0.53
56:Aa:16:GLY:O	56:Aa:17:HIS:ND1	2.42	0.53
67:AQ:140:ARG:NH2	70:B2:1774:C:OP1	2.35	0.53
69:A5:1981:A:OP1	79:Cg:24:ARG:NH1	2.42	0.53
70:B2:1406:A:N6	70:B2:1407:U:O2	2.42	0.53
70:B2:1758:A:O4'	81:AS:85:ASN:CG	2.51	0.53
74:AF:194:THR:N	74:AF:197:GLU:OE2	2.42	0.53
3:CV:84:GLN:HE21	3:CV:86:LYS:HB3	1.74	0.53
6:CN:9:GLU:O	6:CN:13:LYS:NZ	2.42	0.53
9:CQ:65:ARG:HE	69:A5:872:A:H2'	1.74	0.53
11:CA:108:PRO:HG3	32:Cp:90:LYS:HD2	1.90	0.53
14:CP:67:VAL:HA	14:CP:82:ARG:HH21	1.74	0.53
18:Cr:107:ARG:NH2	69:A5:489:U:O2'	2.42	0.53
21:CB:375:GLY:HA2	69:A5:3621:A:H4'	1.90	0.53
43:AO:50:ARG:HD3	51:AB:65:ARG:HH11	1.74	0.53
48:AL:86:ARG:NH1	48:AL:88:ASP:OD1	2.42	0.53
55:AZ:51:LYS:CG	81:AS:6:PRO:HB3	2.15	0.53
69:A5:186:G:N2	69:A5:187:A:N7	2.46	0.53
69:A5:1931:C:N4	69:A5:1935:G:OP2	2.40	0.53
8:CD:136:ASP:N	8:CD:136:ASP:OD1	2.41	0.52
11:CA:67:TYR:OH	69:A5:2919:A:N7	2.40	0.52
20:Cb:43:GLN:N	69:A5:1289:C:N3	2.57	0.52
21:CB:59:GLU:HA	21:CB:71:GLU:HA	1.91	0.52
54:AY:9:ARG:HD2	70:B2:863:A:H4'	1.91	0.52
62:AE:29:PRO:HA	70:B2:453:C:H5'	1.91	0.52
68:Cz:4:LYS:HE3	68:Cz:9:THR:H	1.74	0.52
69:A5:2506:U:O2'	69:A5:2679:U:OP1	2.22	0.52
8:CD:267:ARG:HH21	39:A7:120:U:H2'	1.75	0.52
11:CA:68:ARG:HB3	11:CA:70:LYS:HE3	1.91	0.52
17:CZ:48:ARG:HB3	17:CZ:69:LYS:HB3	1.91	0.52
34:CJ:95:ARG:NH2	34:CJ:113:GLY:O	2.40	0.52
56:Aa:14:ASN:O	70:B2:1024:C:N4	2.30	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:AJ:86:GLY:HA3	61:AJ:152:LEU:HD13	1.91	0.52
61:AJ:144:ASN:H	70:B2:849:U:H5	1.57	0.52
69:A5:889:G:H22	69:A5:899:G:H22	1.56	0.52
69:A5:1577:A:N6	69:A5:1581:G:O6	2.43	0.52
70:B2:108:G:O2'	70:B2:881:U:O4	2.27	0.52
70:B2:1390:U:N3	70:B2:1408:A:O2'	2.42	0.52
7:CI:88:ARG:NH2	7:CI:195:CYS:SG	2.82	0.52
35:CH:23:ARG:HD2	35:CH:39:LYS:HA	1.90	0.52
36:CE:74:PHE:HB3	36:CE:76:LYS:HE3	1.92	0.52
52:AA:36:GLN:NE2	53:AV:67:ASP:OD2	2.42	0.52
66:AI:143:ARG:NH2	70:B2:188:C:OP2	2.42	0.52
69:A5:163:A:OP1	69:A5:165:G:O2'	2.26	0.52
70:B2:601:U:H4'	70:B2:603:G:H4'	1.90	0.52
74:AF:170:LEU:O	74:AF:174:ASN:ND2	2.42	0.52
3:CV:15:ARG:HB2	69:A5:3576:G:H5''	1.91	0.52
21:CB:329:ASP:N	21:CB:329:ASP:OD1	2.34	0.52
23:Cc:30:GLY:O	23:Cc:34:THR:OG1	2.22	0.52
36:CE:102:ILE:HG12	36:CE:112:ARG:HG2	1.91	0.52
61:AJ:126:HIS:ND1	70:B2:483:A:O2'	2.29	0.52
66:AI:22:ARG:NH1	70:B2:307:U:OP1	2.42	0.52
69:A5:3221:A:N6	69:A5:3234:A:O2'	2.41	0.52
37:CG:86:HIS:HB2	37:CG:242:TRP:CE2	2.44	0.52
37:CG:107:TYR:HB3	37:CG:140:TYR:HA	1.91	0.52
41:Ag:21:ILE:HG21	41:Ag:308:ILE:HD12	1.91	0.52
46:Ad:19:ARG:NH2	70:B2:1789:A:OP1	2.42	0.52
50:AP:78:ILE:HD12	50:AP:96:ILE:HG12	1.91	0.52
51:AB:174:ILE:HD11	51:AB:200:ILE:HG13	1.92	0.52
60:Af:81:LYS:NZ	70:B2:1624:U:O4	2.42	0.52
64:AG:176:LYS:HE2	70:B2:65:A:H5'	1.92	0.52
69:A5:1912:G:OP1	69:A5:1922:A:N6	2.43	0.52
70:B2:905:U:H1'	70:B2:940:U:H3	1.73	0.52
37:CG:32:VAL:O	37:CG:35:GLN:NE2	2.40	0.52
47:AN:71:ILE:HD12	70:B2:1048:U:H5''	1.91	0.52
56:Aa:76:SER:HB3	70:B2:1988:G:H22	1.75	0.52
57:Ab:56:CYS:H	57:Ab:60:ALA:HA	1.74	0.52
65:AH:63:PRO:HA	65:AH:95:GLU:HB2	1.92	0.52
69:A5:30:A:N3	69:A5:346:U:O2'	2.39	0.52
69:A5:749:U:H6	69:A5:752:U:H1'	1.74	0.52
69:A5:2639:G:O2'	69:A5:2641:C:N4	2.43	0.52
69:A5:3430:G:H5''	69:A5:3431:C:H5'	1.92	0.52
69:A5:3593:A:P	80:Cd:35:PHE:HZ	2.32	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:A5:3755:A:C8	69:A5:3756:A:H1'	2.44	0.52
8:CD:221:ARG:HH22	39:A7:50:A:H1'	1.75	0.52
11:CA:14:SER:OG	11:CA:15:VAL:N	2.43	0.52
14:CP:184:ARG:NH2	69:A5:3703:C:OP2	2.43	0.52
22:CF:190:CYS:SG	22:CF:191:VAL:N	2.83	0.52
34:CJ:68:ARG:NE	34:CJ:71:GLU:OE2	2.38	0.52
51:AB:106:MET:HE1	51:AB:215:ILE:HB	1.92	0.52
55:AZ:48:LEU:HG	81:AS:7:GLU:CB	2.40	0.52
64:AG:4:ASN:HA	64:AG:15:LEU:HA	1.91	0.52
70:B2:1695:A:C5	81:AS:82:TRP:CG	2.96	0.52
81:AS:51:ASP:N	81:AS:51:ASP:OD1	2.40	0.52
19:Ch:51:ARG:NH1	40:A8:48:G:OP2	2.42	0.52
30:Cm:100:TYR:O	69:A5:3427:G:O2'	2.24	0.52
49:AR:71:ILE:HG13	49:AR:73:LEU:H	1.74	0.52
52:AA:200:ASP:HB2	52:AA:203:PHE:HB2	1.90	0.52
55:AZ:103:HIS:ND1	70:B2:1722:U:OP2	2.43	0.52
63:AC:114:GLY:HA3	63:AC:199:MET:HB3	1.91	0.52
68:Cz:103:LEU:HG	68:Cz:105:LYS:H	1.75	0.52
69:A5:568:A:O2'	69:A5:640:U:O4	2.27	0.52
69:A5:1978:G:H5'	69:A5:2055:G:H21	1.75	0.52
69:A5:1991:A:OP1	76:CU:272:ARG:NH1	2.43	0.52
69:A5:3675:A:C5	69:A5:3678:G:H1'	2.44	0.52
70:B2:1879:U:O2	70:B2:1910:U:N3	2.43	0.52
73:AK:38:ILE:HD12	73:AK:42:HIS:HB3	1.91	0.52
7:CI:196:ASN:OD1	7:CI:196:ASN:N	2.43	0.52
8:CD:21:ARG:HG3	8:CD:24:ARG:HH21	1.74	0.52
11:CA:208:GLU:OE2	69:A5:1112:G:N2	2.29	0.52
12:CS:63:SER:O	12:CS:63:SER:OG	2.26	0.52
12:CS:170:ARG:NE	69:A5:3757:U:O2'	2.43	0.52
21:CB:120:LYS:NZ	69:A5:3536:U:OP1	2.33	0.52
29:CC:382:ALA:O	69:A5:696:U:O2'	2.27	0.52
41:Ag:43:TRP:HA	41:Ag:56:PRO:HA	1.91	0.52
69:A5:2134:A:H2'	69:A5:2136:U:H1'	1.92	0.52
69:A5:3712:G:H4'	69:A5:3775:A:H2'	1.92	0.52
70:B2:1758:A:O4'	81:AS:85:ASN:ND2	2.42	0.52
1:CO:201:TYR:HB2	1:CO:205:VAL:HG21	1.91	0.52
2:CL:152:PRO:HB2	2:CL:153:VAL:HG23	1.92	0.52
7:CI:54:SER:HB2	7:CI:135:ILE:HD11	1.91	0.52
14:CP:142:SER:O	14:CP:142:SER:OG	2.24	0.52
23:Cc:28:CYS:HB3	23:Cc:33:GLN:HB3	1.92	0.52
24:Cc:25:ASP:OD1	24:Cc:25:ASP:N	2.33	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:CE:177:LYS:HB3	36:CE:179:THR:HG23	1.92	0.52
48:AL:39:LEU:HD13	70:B2:251:G:H1'	1.92	0.52
49:AR:82:ASP:HA	52:AA:205:ARG:HH22	1.75	0.52
52:AA:155:ARG:NH1	53:AV:61:ARG:O	2.43	0.52
54:AY:106:LYS:NZ	70:B2:464:G:O6	2.42	0.52
63:AC:52:LEU:HD11	63:AC:256:LEU:HD21	1.91	0.52
66:AI:207:LYS:NZ	69:A5:2262:A:OP1	2.43	0.52
69:A5:707:C:H2'	69:A5:708:A:H8	1.75	0.52
73:AK:43:VAL:O	73:AK:48:GLN:N	2.41	0.52
2:CL:197:LYS:NZ	69:A5:3313:U:O3'	2.40	0.51
10:CR:186:ALA:HA	10:CR:189:ALA:HB3	1.91	0.51
11:CA:77:ILE:HD12	11:CA:128:ARG:HB2	1.91	0.51
36:CE:23:ASN:O	36:CE:25:TYR:N	2.42	0.51
41:Ag:287:CYS:HA	41:Ag:303:TYR:HA	1.91	0.51
52:AA:174:MET:HA	52:AA:177:LEU:HB2	1.90	0.51
58:AD:118:ARG:NH1	63:AC:129:GLU:OE1	2.42	0.51
60:Af:95:ARG:NH1	70:B2:1335:C:OP2	2.43	0.51
69:A5:214:A:N3	69:A5:240:G:O2'	2.43	0.51
69:A5:2268:G:O2'	69:A5:2474:A:N1	2.40	0.51
70:B2:1344:A:H2'	73:AK:8:ARG:HH21	1.75	0.51
70:B2:1750:U:O4'	81:AS:124:ARG:NH1	2.43	0.51
6:CN:159:ARG:HB2	6:CN:164:LEU:HB2	1.91	0.51
7:CI:38:ARG:NH2	7:CI:45:ASP:OD2	2.41	0.51
12:CS:176:PHE:HE1	69:A5:3752:G:H5'	1.74	0.51
29:CC:118:VAL:HB	29:CC:123:ARG:HE	1.76	0.51
32:Cp:31:ILE:O	32:Cp:35:SER:OG	2.23	0.51
52:AA:41:ARG:NH1	52:AA:47:ASN:OD1	2.44	0.51
54:AY:24:MET:HE1	54:AY:45:LEU:HD21	1.91	0.51
64:AG:220:GLU:O	64:AG:224:LYS:N	2.43	0.51
68:Cz:26:ARG:NH2	69:A5:2848:A:O2'	2.42	0.51
69:A5:458:A:N6	69:A5:761:C:O2'	2.39	0.51
69:A5:1418:A:H2'	69:A5:1419:A:C8	2.45	0.51
69:A5:1879:U:OP2	79:Cg:36:LYS:NZ	2.42	0.51
69:A5:2145:G:H5''	69:A5:2146:G:H5'	1.91	0.51
69:A5:3593:A:C5'	80:Cd:35:PHE:CZ	2.92	0.51
70:B2:1210:G:N2	70:B2:1213:A:OP2	2.43	0.51
5:Ca:76:LEU:HG	5:Ca:114:GLY:HA2	1.93	0.51
22:CF:27:LYS:HG3	22:CF:29:ILE:HG12	1.91	0.51
37:CG:195:LEU:HB2	37:CG:204:CYS:HB3	1.91	0.51
41:Ag:253:TYR:OH	41:Ag:270:GLU:OE1	2.27	0.51
55:AZ:50:ASP:N	81:AS:7:GLU:H	2.03	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:Aa:93:ARG:NH1	70:B2:1166:U:OP1	2.44	0.51
61:AJ:88:LEU:HB2	61:AJ:101:LEU:HD11	1.91	0.51
65:AH:116:ARG:NH1	70:B2:646:U:O4'	2.44	0.51
69:A5:2477:C:H2'	69:A5:2478:A:H8	1.75	0.51
70:B2:43:A:H1'	70:B2:383:A:H1'	1.92	0.51
70:B2:1695:A:C8	81:AS:83:PHE:CZ	2.99	0.51
11:CA:104:LEU:HD11	11:CA:113:ILE:HD13	1.92	0.51
19:Ch:10:ARG:O	19:Ch:64:LYS:NZ	2.42	0.51
22:CF:246:ARG:HH12	69:A5:648:U:H5''	1.76	0.51
35:CH:98:PRO:O	35:CH:114:ASN:ND2	2.43	0.51
35:CH:184:THR:OG1	35:CH:187:LYS:O	2.27	0.51
36:CE:200:LYS:NZ	36:CE:204:GLU:OE1	2.43	0.51
36:CE:237:TYR:HB2	36:CE:241:MET:HG3	1.93	0.51
41:Ag:272:ARG:NH1	41:Ag:274:GLU:OE1	2.43	0.51
62:AE:18:TRP:O	62:AE:51:ARG:NH2	2.42	0.51
64:AG:173:LYS:NZ	70:B2:66:C:O3'	2.43	0.51
65:AH:138:VAL:HG21	65:AH:157:ASP:HB2	1.92	0.51
67:AQ:2:GLN:HA	67:AQ:5:ARG:HG3	1.93	0.51
69:A5:1518:A:N3	69:A5:3417:C:O2'	2.39	0.51
29:CC:89:ARG:O	29:CC:92:GLN:HB2	2.11	0.51
40:A8:6:U:H2'	40:A8:7:A:C8	2.46	0.51
55:AZ:61:VAL:HA	55:AZ:64:TYR:HB2	1.91	0.51
69:A5:1316:U:N3	69:A5:1318:A:OP1	2.43	0.51
69:A5:3477:A:H5''	69:A5:3478:G:H5'	1.93	0.51
70:B2:29:U:H2'	70:B2:30:G:H8	1.75	0.51
70:B2:1114:A:OP1	70:B2:1984:G:O2'	2.24	0.51
70:B2:1750:U:N1	81:AS:124:ARG:HD3	2.26	0.51
2:CL:11:GLN:HE22	9:CQ:168:ARG:HH22	1.59	0.51
7:CI:213:GLN:HA	7:CI:216:VAL:HG12	1.92	0.51
14:CP:64:ASN:ND2	69:A5:2766:U:O5'	2.43	0.51
17:CZ:95:LEU:O	17:CZ:109:HIS:NE2	2.40	0.51
23:Cc:55:LEU:HD11	79:Cg:91:ARG:HB2	1.91	0.51
51:AB:231:LEU:O	51:AB:235:HIS:N	2.43	0.51
61:AJ:126:HIS:HD1	70:B2:483:A:HO2'	1.54	0.51
65:AH:55:LYS:HE2	65:AH:88:LYS:HA	1.91	0.51
69:A5:1193:A:C2	69:A5:1277:A:H2'	2.45	0.51
69:A5:2200:A:OP2	80:Cd:41:ARG:NH2	2.44	0.51
69:A5:3132:C:H2'	69:A5:3133:A:H8	1.76	0.51
70:B2:719:G:H22	70:B2:818:C:H2'	1.76	0.51
70:B2:1668:A:N3	72:AT:48:TYR:OH	2.43	0.51
78:CW:50:THR:O	78:CW:61:LYS:NZ	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Cr:76:ARG:HB2	18:Cr:78:ALA:H	1.73	0.51
50:AP:127:LYS:HD2	70:B2:1270:U:H4'	1.91	0.51
69:A5:1784:A:N3	69:A5:1785:G:H5'	2.25	0.51
69:A5:1863:U:OP2	69:A5:2916:U:N3	2.43	0.51
70:B2:225:G:O3'	70:B2:228:A:N6	2.44	0.51
70:B2:492:G:H1	70:B2:507:C:H1'	1.74	0.51
70:B2:1739:U:O2'	81:AS:88:LYS:O	2.28	0.51
5:Ca:76:LEU:HB2	5:Ca:116:GLY:HA2	1.91	0.51
9:CQ:95:VAL:HG21	9:CQ:112:ARG:HB3	1.93	0.51
21:CB:252:ALA:HB1	69:A5:3478:G:N3	2.26	0.51
42:AU:65:ILE:HB	42:AU:82:PHE:HB2	1.91	0.51
57:Ab:55:VAL:HB	57:Ab:60:ALA:HB1	1.92	0.51
64:AG:33:GLY:HA2	64:AG:51:ARG:HE	1.75	0.51
69:A5:1026:G:OP1	69:A5:1874:G:O2'	2.29	0.51
69:A5:3163:U:O2'	69:A5:3229:A:N3	2.39	0.51
70:B2:320:A:N1	70:B2:354:U:O2'	2.44	0.51
70:B2:1257:G:N1	70:B2:1767:G:OP2	2.40	0.51
70:B2:1695:A:C6	81:AS:82:TRP:CD1	2.94	0.51
9:CQ:11:ARG:HG3	69:A5:1557:U:H5''	1.93	0.51
9:CQ:102:ALA:HB3	9:CQ:105:VAL:HG23	1.92	0.51
15:CX:165:VAL:HG11	69:A5:2917:A:H3'	1.93	0.51
39:A7:58:A:H2'	39:A7:59:G:H8	1.75	0.51
47:AN:34:LYS:NZ	47:AN:77:SER:OG	2.44	0.51
63:AC:97:LYS:HA	70:B2:10:G:H21	1.76	0.51
65:AH:75:ILE:HD11	65:AH:134:PRO:HG3	1.93	0.51
69:A5:478:A:O2'	69:A5:527:U:O2	2.26	0.51
69:A5:1267:A:H5''	69:A5:3169:A:H61	1.76	0.51
69:A5:3789:U:H3	69:A5:3823:G:H22	1.57	0.51
70:B2:5:U:O2'	70:B2:561:G:O3'	2.27	0.51
70:B2:1304:G:O2'	70:B2:1636:A:N6	2.44	0.51
70:B2:1444:C:O2'	70:B2:1536:A:N6	2.44	0.51
70:B2:1758:A:OP1	81:AS:37:GLY:C	2.52	0.51
6:CN:143:ARG:O	6:CN:149:ASN:ND2	2.44	0.51
35:CH:111:GLU:OE2	35:CH:123:ARG:NH1	2.44	0.51
41:Ag:258:LYS:HD2	41:Ag:260:TRP:CE2	2.46	0.51
45:AM:35:ALA:HB1	45:AM:120:ASP:HB2	1.93	0.51
50:AP:20:TYR:C	81:AS:90:ILE:O	2.54	0.51
69:A5:1115:A:O2'	69:A5:2516:U:O2	2.24	0.51
69:A5:3686:A:H1'	69:A5:3868:G:C5	2.46	0.51
70:B2:1672:A:H5'	72:AT:11:GLN:HG2	1.93	0.51
74:AF:141:ALA:O	74:AF:145:SER:N	2.38	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CL:104:LYS:HG3	69:A5:78:A:H5''	1.92	0.50
9:CQ:133:GLY:O	9:CQ:136:THR:OG1	2.24	0.50
35:CH:91:ARG:NH1	35:CH:141:GLU:OE2	2.43	0.50
37:CG:264:ARG:HA	37:CG:267:ALA:HB3	1.93	0.50
42:AU:81:ARG:NH2	70:B2:1797:G:OP1	2.44	0.50
67:AQ:60:LEU:HA	67:AQ:64:LYS:HG3	1.92	0.50
69:A5:1193:A:C8	69:A5:1309:U:H2'	2.46	0.50
70:B2:1028:A:O2'	70:B2:1112:A:N6	2.44	0.50
78:CW:52:THR:OG1	78:CW:53:VAL:N	2.44	0.50
7:CI:149:ILE:HG23	7:CI:165:ILE:HG21	1.93	0.50
7:CI:196:ASN:HD22	69:A5:1255:U:H5'	1.76	0.50
33:Co:54:PRO:HB3	69:A5:3334:A:H5'	1.93	0.50
50:AP:15:PHE:HD1	50:AP:17:LYS:H	1.59	0.50
62:AE:246:LEU:HD12	62:AE:251:GLU:HB2	1.93	0.50
69:A5:1551:U:H2'	69:A5:1552:A:C8	2.46	0.50
70:B2:1695:A:N1	81:AS:82:TRP:CE2	2.79	0.50
3:CV:21:PRO:HA	3:CV:54:ALA:HA	1.93	0.50
8:CD:150:LEU:HB2	34:CJ:151:ARG:CZ	2.41	0.50
9:CQ:183:SER:OG	69:A5:3322:A:OP2	2.30	0.50
26:CI:60:HIS:HB3	26:CI:64:GLU:HB2	1.93	0.50
56:Aa:23:CYS:HB3	56:Aa:28:ARG:H	1.76	0.50
57:Ab:12:PRO:HB2	65:AH:192:LEU:HD23	1.92	0.50
59:Ae:113:ARG:HH21	61:AJ:31:LYS:HD3	1.76	0.50
61:AJ:6:ILE:HG21	70:B2:840:U:H4'	1.94	0.50
61:AJ:29:GLU:HB2	61:AJ:44:VAL:HG11	1.94	0.50
64:AG:22:HIS:HA	64:AG:25:ARG:HG3	1.94	0.50
65:AH:104:ARG:NH2	65:AH:105:LYS:O	2.44	0.50
66:AI:23:LYS:HE2	70:B2:391:G:H5''	1.92	0.50
67:AQ:136:GLY:HA3	67:AQ:142:ARG:HA	1.93	0.50
69:A5:602:A:H5''	69:A5:611:C:H5''	1.94	0.50
69:A5:3789:U:H3	69:A5:3823:G:H1	1.58	0.50
69:A5:3819:C:OP1	69:A5:3821:G:N2	2.44	0.50
70:B2:1013:A:OP1	70:B2:1103:U:O2'	2.28	0.50
70:B2:1205:U:H2'	70:B2:1206:G:C8	2.46	0.50
72:AT:121:ARG:HH11	72:AT:123:LEU:HD23	1.75	0.50
4:CM:53:ASN:OD1	12:CS:156:GLN:NE2	2.41	0.50
6:CN:83:LYS:NZ	69:A5:50:U:O4	2.44	0.50
22:CF:114:LEU:O	69:A5:1313:A:O2'	2.28	0.50
34:CJ:23:ARG:NH2	34:CJ:145:ASN:OD1	2.44	0.50
39:A7:11:A:O2'	39:A7:13:A:OP2	2.27	0.50
41:Ag:250:CYS:HA	41:Ag:259:ILE:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:AL:34:SER:OG	48:AL:47:ALA:O	2.29	0.50
48:AL:63:VAL:HG11	48:AL:131:LEU:HD21	1.92	0.50
55:AZ:50:ASP:OD1	81:AS:8:LYS:HE3	2.12	0.50
63:AC:91:LYS:HB3	63:AC:110:PHE:HB2	1.93	0.50
65:AH:5:SER:OG	65:AH:6:LYS:N	2.43	0.50
69:A5:1930:G:N2	69:A5:1938:C:O2	2.44	0.50
69:A5:2404:U:H5''	69:A5:2405:A:H5'	1.94	0.50
69:A5:2853:A:N6	69:A5:2863:U:O4	2.43	0.50
69:A5:3712:G:H3'	69:A5:3713:C:H2'	1.93	0.50
69:A5:3713:C:O2'	69:A5:3768:C:O2	2.29	0.50
74:AF:56:ILE:HG23	74:AF:136:GLN:HE21	1.75	0.50
1:CO:38:VAL:HB	1:CO:110:ILE:HB	1.93	0.50
5:Ca:14:GLY:HA3	69:A5:1143:U:H3'	1.94	0.50
11:CA:102:MET:HE3	11:CA:107:MET:HG2	1.92	0.50
16:CY:23:SER:O	16:CY:75:ARG:NH1	2.44	0.50
36:CE:85:SER:OG	69:A5:749:U:O4	2.29	0.50
49:AR:78:ARG:HH12	49:AR:82:ASP:HB3	1.77	0.50
50:AP:111:LYS:HD2	50:AP:112:PRO:HD2	1.92	0.50
66:AI:148:MET:SD	66:AI:148:MET:N	2.80	0.50
69:A5:1790:A:H2'	69:A5:1791:A:C8	2.47	0.50
69:A5:3247:A:H5''	69:A5:3247:A:H8	1.77	0.50
70:B2:51:A:OP2	70:B2:429:C:N4	2.45	0.50
70:B2:1638:A:O2'	70:B2:1640:G:N7	2.41	0.50
2:CL:163:VAL:HG21	5:Ca:106:LYS:HD3	1.93	0.50
29:CC:383:LYS:NZ	69:A5:697:U:OP1	2.44	0.50
35:CH:50:LYS:HB2	35:CH:52:THR:HG22	1.93	0.50
43:AO:108:PRO:HD2	56:Aa:67:LEU:HD11	1.93	0.50
53:AV:19:ALA:O	71:AW:23:ARG:NH1	2.44	0.50
69:A5:2584:G:H5''	69:A5:2585:A:H2	1.76	0.50
70:B2:222:C:N4	70:B2:239:G:OP2	2.44	0.50
70:B2:905:U:H5''	70:B2:935:A:H61	1.77	0.50
9:CQ:103:LEU:HD22	29:CC:286:LYS:HD3	1.93	0.50
15:CX:226:ASN:O	15:CX:228:ASN:N	2.41	0.50
25:Cf:102:LYS:HE2	69:A5:453:C:H41	1.76	0.50
29:CC:9:LEU:HD22	29:CC:24:ASN:HB3	1.93	0.50
29:CC:314:ARG:NH2	69:A5:750:G:OP1	2.44	0.50
34:CJ:20:LEU:HD13	34:CJ:162:LEU:HD22	1.94	0.50
36:CE:93:ARG:NH1	36:CE:142:GLN:O	2.40	0.50
41:Ag:105:HIS:ND1	41:Ag:108:ASP:O	2.44	0.50
57:Ab:23:ARG:NH1	57:Ab:25:VAL:O	2.37	0.50
63:AC:78:ASP:OD1	63:AC:78:ASP:N	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:AQ:2:GLN:NE2	70:B2:1565:C:OP2	2.33	0.50
67:AQ:147:TYR:HH	70:B2:1655:C:HO2'	1.59	0.50
68:Cz:26:ARG:NH1	68:Cz:28:PHE:O	2.44	0.50
69:A5:1981:A:H61	69:A5:2091:A:H61	1.59	0.50
69:A5:2482:C:H2'	69:A5:2483:A:H8	1.77	0.50
14:CP:168:LYS:NZ	69:A5:768:U:O2'	2.45	0.50
42:AU:22:ILE:HD13	42:AU:93:LEU:HD23	1.93	0.50
45:AM:63:PHE:HE2	45:AM:68:TYR:HB3	1.77	0.50
46:Ad:12:ARG:NH1	70:B2:1293:C:O2'	2.45	0.50
56:Aa:32:LYS:NZ	70:B2:1017:A:OP1	2.45	0.50
60:Af:136:GLU:O	60:Af:138:ARG:N	2.44	0.50
61:AJ:122:LYS:HE2	70:B2:484:C:H4'	1.92	0.50
62:AE:3:ARG:HG2	70:B2:92:A:H1'	1.93	0.50
62:AE:105:VAL:HA	62:AE:190:GLY:HA3	1.93	0.50
63:AC:177:ARG:NH1	70:B2:615:G:H1	2.10	0.50
64:AG:79:LYS:HD2	64:AG:80:GLY:HA2	1.93	0.50
68:Cz:98:LYS:HG3	68:Cz:104:ALA:HA	1.92	0.50
69:A5:468:U:O4	69:A5:533:A:N6	2.45	0.50
69:A5:1888:A:H4'	69:A5:2151:A:H4'	1.93	0.50
69:A5:2200:A:P	80:Cd:41:ARG:HH22	2.35	0.50
69:A5:2574:C:O2'	69:A5:2648:A:N3	2.43	0.50
69:A5:3194:A:H2'	69:A5:3195:G:H8	1.77	0.50
69:A5:3717:U:H3	69:A5:3760:A:H61	1.59	0.50
70:B2:1653:C:H2'	70:B2:1654:G:H8	1.77	0.50
10:CR:191:GLU:OE1	65:AH:40:ARG:NH2	2.45	0.50
54:AY:84:LYS:HG2	54:AY:92:LEU:HD11	1.94	0.50
55:AZ:110:ARG:HE	55:AZ:112:THR:HG23	1.77	0.50
56:Aa:95:ARG:O	70:B2:1992:A:O2'	2.29	0.50
58:AD:139:VAL:HG22	58:AD:153:LYS:HG2	1.94	0.50
60:Af:151:SER:HB2	60:Af:152:LYS:HG3	1.94	0.50
61:AJ:112:GLN:O	61:AJ:128:ARG:NH2	2.45	0.50
70:B2:1169:C:H42	71:AW:20:ARG:HH11	1.59	0.50
75:Ac:39:ILE:O	75:Ac:40:ARG:NH1	2.40	0.50
11:CA:40:TYR:HA	11:CA:91:GLY:HA3	1.94	0.49
12:CS:95:ARG:NH2	69:A5:1427:G:O2'	2.45	0.49
30:Cm:104:HIS:CD2	30:Cm:111:ARG:HH12	2.29	0.49
62:AE:125:LYS:HA	62:AE:159:SER:HA	1.94	0.49
67:AQ:99:GLN:HA	67:AQ:107:LYS:HZ1	1.77	0.49
69:A5:1447:C:N4	69:A5:1477:G:OP2	2.40	0.49
69:A5:2517:A:O2'	77:Cj:2:THR:N	2.45	0.49
70:B2:1275:U:H2'	70:B2:1276:G:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:B2:1649:U:C1'	81:AS:135:HIS:CD2	2.95	0.49
72:AT:126:ILE:HD12	72:AT:131:LEU:HD21	1.92	0.49
74:AF:85:LYS:HD2	74:AF:87:PHE:H	1.76	0.49
74:AF:171:ARG:HH22	75:Ac:22:GLN:HG3	1.75	0.49
5:Ca:112:LEU:HD22	5:Ca:125:VAL:HG11	1.94	0.49
10:CR:168:GLU:HA	10:CR:170:ARG:HH11	1.76	0.49
36:CE:218:GLU:HG3	36:CE:223:ALA:HB3	1.93	0.49
47:AN:76:LYS:O	70:B2:898:U:N3	2.45	0.49
52:AA:66:VAL:HG11	52:AA:185:LEU:HB3	1.94	0.49
55:AZ:52:ALA:O	55:AZ:56:LYS:NZ	2.45	0.49
58:AD:64:LYS:O	58:AD:69:ARG:NH2	2.45	0.49
58:AD:160:ILE:HG21	58:AD:165:PRO:HB2	1.94	0.49
62:AE:125:LYS:HG2	62:AE:142:HIS:HB3	1.94	0.49
64:AG:154:ARG:HH21	70:B2:76:A:H5'	1.77	0.49
64:AG:169:LYS:HB2	70:B2:73:A:H62	1.77	0.49
78:CW:56:ARG:NE	78:CW:61:LYS:HD2	2.26	0.49
11:CA:223:SER:HG	69:A5:2622:A:HO2'	1.59	0.49
13:CT:69:GLN:NE2	69:A5:3270:G:OP1	2.45	0.49
16:CY:126:ARG:NE	69:A5:202:A:OP1	2.45	0.49
24:Ce:20:ILE:HG23	24:Ce:32:HIS:HB2	1.93	0.49
29:CC:344:LEU:HD11	36:CE:31:LEU:HD13	1.94	0.49
34:CJ:19:ASP:H	34:CJ:142:PRO:HD2	1.77	0.49
36:CE:30:ILE:O	36:CE:32:ARG:NH2	2.45	0.49
37:CG:254:ARG:NH2	69:A5:2907:U:OP1	2.44	0.49
40:A8:40:A:H4'	77:Cj:59:THR:HG23	1.93	0.49
43:AO:100:THR:O	43:AO:100:THR:OG1	2.26	0.49
45:AM:62:SER:OG	45:AM:87:ASP:O	2.25	0.49
51:AB:118:LYS:O	51:AB:121:GLN:NE2	2.45	0.49
69:A5:1687:U:H5	69:A5:2735:A:H62	1.61	0.49
69:A5:3529:A:C6	69:A5:3531:C:H4'	2.48	0.49
70:B2:522:G:H1	70:B2:551:C:H42	1.60	0.49
70:B2:1314:G:O3'	70:B2:1316:G:N2	2.44	0.49
72:AT:11:GLN:HB2	72:AT:15:THR:HG23	1.94	0.49
13:CT:63:ARG:NH2	69:A5:1274:A:OP1	2.46	0.49
25:Cf:47:HIS:O	69:A5:3714:U:O2'	2.27	0.49
30:Cm:86:ALA:HB2	35:CH:93:VAL:HG11	1.93	0.49
32:Cp:23:ARG:NH2	69:A5:2241:U:O2'	2.45	0.49
52:AA:89:LYS:HD2	52:AA:202:PHE:HA	1.95	0.49
63:AC:47:THR:HG23	63:AC:50:GLY:H	1.77	0.49
70:B2:1090:A:O2'	70:B2:1092:A:N7	2.40	0.49
70:B2:1170:G:HO2'	70:B2:1181:G:HO2'	1.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:AS:121:ARG:O	81:AS:125:HIS:ND1	2.41	0.49
2:CL:187:THR:HA	2:CL:190:ARG:HB3	1.95	0.49
34:CJ:169:LYS:O	34:CJ:172:GLN:NE2	2.45	0.49
35:CH:84:PHE:HA	35:CH:186:VAL:HG12	1.94	0.49
41:Ag:153:SER:HB2	41:Ag:169:CYS:HB2	1.94	0.49
62:AE:86:TYR:OH	62:AE:182:MET:SD	2.69	0.49
67:AQ:1:MET:HG3	67:AQ:2:GLN:HG2	1.93	0.49
69:A5:1637:U:H2'	69:A5:1638:G:C8	2.46	0.49
70:B2:253:A:O2'	70:B2:255:U:OP1	2.30	0.49
72:AT:40:ALA:HA	72:AT:96:ALA:HB3	1.95	0.49
23:Cc:35:LEU:HD13	23:Cc:63:TYR:HE2	1.77	0.49
26:Ci:73:VAL:HG11	69:A5:2823:A:H4'	1.94	0.49
37:CG:148:VAL:HG13	37:CG:208:ALA:HB2	1.95	0.49
41:Ag:167:VAL:HG23	41:Ag:177:VAL:HG22	1.95	0.49
42:AU:36:ASN:O	42:AU:40:ASP:N	2.43	0.49
42:AU:109:GLU:O	58:AD:42:ARG:NH1	2.46	0.49
46:Ad:33:LYS:HD3	70:B2:1786:G:H5'	1.94	0.49
55:AZ:45:ASN:ND2	55:AZ:78:ILE:O	2.46	0.49
67:AQ:80:VAL:HG12	70:B2:1801:U:H5''	1.95	0.49
69:A5:433:U:H2'	69:A5:434:A:H8	1.78	0.49
69:A5:2034:U:O2'	69:A5:2036:G:N7	2.39	0.49
69:A5:2069:U:H3	69:A5:2083:G:H22	1.60	0.49
70:B2:1079:A:O2'	70:B2:1980:U:O2	2.26	0.49
2:CL:62:THR:HG21	5:Ca:67:GLN:NE2	2.28	0.49
8:CD:116:ASP:OD1	8:CD:116:ASP:N	2.45	0.49
18:Cr:50:LYS:HB3	18:Cr:72:LYS:HA	1.94	0.49
32:Cp:48:LYS:NZ	69:A5:2103:G:OP1	2.45	0.49
34:CJ:62:VAL:HG12	34:CJ:67:ILE:HG12	1.94	0.49
35:CH:51:ARG:HH11	69:A5:592:G:H5''	1.77	0.49
47:AN:76:LYS:HB3	47:AN:81:LYS:HB3	1.93	0.49
51:AB:39:PHE:HD2	51:AB:40:GLN:HB2	1.78	0.49
57:Ab:62:ILE:HG23	57:Ab:74:THR:HG21	1.94	0.49
66:AI:145:GLU:N	70:B2:189:C:N3	2.50	0.49
69:A5:826:A:O2'	69:A5:828:G:O2'	2.30	0.49
69:A5:1474:A:N3	69:A5:1495:C:O2'	2.43	0.49
69:A5:2647:U:H1'	69:A5:2649:A:H2	1.78	0.49
70:B2:626:U:H3	70:B2:1173:A:H61	1.60	0.49
70:B2:1448:A:OP1	70:B2:1451:A:N6	2.45	0.49
74:AF:176:ALA:HA	74:AF:179:LEU:HD12	1.93	0.49
81:AS:86:ARG:HH12	81:AS:106:LYS:HE2	1.77	0.49
18:Cr:58:ALA:H	18:Cr:59:ALA:HA	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:CC:29:ALA:HB1	29:CC:270:TRP:CD1	2.48	0.49
34:CJ:38:LEU:HD23	34:CJ:75:VAL:HG23	1.94	0.49
50:AP:108:VAL:HG23	81:AS:118:ARG:CZ	2.41	0.49
53:AV:10:ASP:OD1	53:AV:10:ASP:N	2.46	0.49
56:Aa:88:SER:O	56:Aa:92:ARG:N	2.46	0.49
60:Af:145:ASN:HD21	70:B2:1320:G:H2'	1.78	0.49
65:AH:49:GLU:HG3	65:AH:58:VAL:HA	1.95	0.49
66:AI:178:SER:HB2	66:AI:189:GLY:HA2	1.94	0.49
68:Cz:207:LYS:NZ	68:Cz:209:SER:OG	2.41	0.49
70:B2:1874:C:H42	70:B2:1914:A:H61	1.61	0.49
6:CN:28:TRP:O	37:CG:71:GLN:NE2	2.42	0.49
11:CA:253:SER:OG	70:B2:1074:G:OP1	2.30	0.49
12:CS:173:ARG:HB3	12:CS:175:TYR:HE1	1.78	0.49
16:CY:19:PHE:O	16:CY:26:ARG:NH2	2.46	0.49
16:CY:56:GLN:HB2	16:CY:67:VAL:HG12	1.94	0.49
22:CF:61:GLN:HG2	29:CC:334:TYR:HE2	1.78	0.49
36:CE:138:ARG:HH21	69:A5:3843:U:H2'	1.78	0.49
57:Ab:46:VAL:HG11	57:Ab:54:VAL:HG11	1.94	0.49
65:AH:50:ILE:HG21	65:AH:174:VAL:HG12	1.95	0.49
66:AI:40:SER:HA	66:AI:61:GLU:HB3	1.95	0.49
69:A5:3108:U:H2'	69:A5:3109:A:H8	1.78	0.49
70:B2:521:U:N3	70:B2:522:G:O6	2.46	0.49
70:B2:990:U:O2'	70:B2:992:A:N7	2.41	0.49
70:B2:1146:U:O2'	70:B2:1147:U:O2	2.30	0.49
70:B2:1175:A:C5	70:B2:1176:C:H1'	2.48	0.49
1:CO:29:LEU:HD21	1:CO:35:VAL:HG22	1.95	0.49
4:CM:134:THR:HG23	4:CM:135:LYS:HG2	1.93	0.49
7:CI:35:ASP:OD1	7:CI:35:ASP:N	2.44	0.49
15:CX:168:ARG:HH21	15:CX:170:PRO:HA	1.78	0.49
21:CB:57:VAL:HB	21:CB:367:PHE:HB3	1.95	0.49
29:CC:175:ARG:HB3	69:A5:225:U:H3'	1.94	0.49
37:CG:205:THR:HG22	37:CG:206:THR:HG22	1.94	0.49
37:CG:219:ASN:OD1	37:CG:219:ASN:N	2.46	0.49
49:AR:71:ILE:HG12	49:AR:74:GLN:HB3	1.93	0.49
50:AP:17:LYS:NZ	50:AP:26:ASP:OD1	2.39	0.49
61:AJ:85:ILE:HA	61:AJ:151:ARG:HA	1.94	0.49
69:A5:490:G:H22	69:A5:510:U:H3	1.60	0.49
69:A5:937:G:H1	69:A5:966:U:H3	1.61	0.49
69:A5:1706:G:O2'	69:A5:1708:G:N7	2.40	0.49
69:A5:2833:U:OP2	69:A5:2878:A:N6	2.43	0.49
69:A5:3221:A:O2'	69:A5:3223:A:N7	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:A5:3401:U:O2'	69:A5:3405:U:OP1	2.28	0.49
70:B2:1411:G:H2'	70:B2:1412:A:H4'	1.94	0.49
73:AK:24:LYS:HG2	73:AK:64:HIS:HA	1.95	0.49
76:CU:204:SER:OG	76:CU:205:ILE:N	2.40	0.49
10:CR:63:VAL:HG21	69:A5:2177:G:H5''	1.95	0.48
21:CB:29:VAL:HG12	21:CB:348:ARG:HH22	1.78	0.48
24:Ce:41:ASP:O	24:Ce:46:ARG:NH1	2.41	0.48
25:Cf:25:LYS:HB3	25:Cf:27:PRO:HG3	1.95	0.48
41:Ag:73:SER:OG	41:Ag:74:SER:N	2.46	0.48
43:AO:147:ARG:O	43:AO:150:ARG:NH1	2.46	0.48
47:AN:50:ILE:HA	47:AN:53:ILE:HG22	1.95	0.48
53:AV:15:ARG:HE	63:AC:67:TYR:HA	1.78	0.48
58:AD:169:TYR:OH	58:AD:205:PRO:O	2.24	0.48
65:AH:55:LYS:HZ1	65:AH:89:HIS:H	1.61	0.48
69:A5:599:C:O3'	69:A5:614:G:N2	2.46	0.48
69:A5:1702:G:H22	69:A5:1715:G:H1	1.61	0.48
69:A5:3712:G:H1'	69:A5:3775:A:H8	1.78	0.48
77:Cj:63:ARG:HD2	77:Cj:65:GLN:HB3	1.95	0.48
79:Cg:23:VAL:HG21	79:Cg:33:GLN:HB2	1.94	0.48
8:CD:56:SER:OG	8:CD:57:ASN:N	2.46	0.48
12:CS:77:ASN:ND2	12:CS:133:PRO:O	2.47	0.48
20:Cb:4:SER:OG	69:A5:1331:G:OP1	2.29	0.48
27:Ck:5:ILE:HG22	27:Ck:7:GLU:H	1.77	0.48
36:CE:22:VAL:HB	36:CE:31:LEU:HD23	1.95	0.48
48:AL:64:ARG:NH1	70:B2:113:G:O3'	2.45	0.48
62:AE:66:MET:SD	62:AE:78:THR:OG1	2.71	0.48
66:AI:36:THR:O	66:AI:36:THR:OG1	2.31	0.48
69:A5:14:C:O2'	69:A5:1801:U:O2	2.25	0.48
69:A5:49:A:O2'	69:A5:99:A:N1	2.44	0.48
69:A5:944:G:H5'	69:A5:945:U:H5'	1.93	0.48
69:A5:1207:G:N2	69:A5:1208:U:O4	2.33	0.48
69:A5:2835:G:H5''	69:A5:2875:A:H2'	1.95	0.48
69:A5:3194:A:H2'	69:A5:3195:G:C8	2.48	0.48
69:A5:3595:U:H2'	69:A5:3596:A:C8	2.48	0.48
1:CO:41:GLU:HG2	1:CO:42:GLU:HG2	1.94	0.48
10:CR:62:ARG:HH12	69:A5:3603:C:H41	1.60	0.48
16:CY:23:SER:HA	16:CY:26:ARG:HB2	1.94	0.48
24:Ce:61:SER:O	24:Ce:66:ARG:NH2	2.45	0.48
29:CC:242:LYS:O	29:CC:251:ARG:NH1	2.40	0.48
36:CE:233:HIS:CG	69:A5:3767:G:H22	2.31	0.48
47:AN:16:LEU:O	71:AW:57:ARG:NH2	2.36	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:AR:86:PRO:HA	49:AR:87:ALA:HA	1.58	0.48
53:AV:35:ASN:HD21	63:AC:247:THR:HG21	1.77	0.48
60:Af:92:LYS:HE2	70:B2:1637:G:H5'	1.96	0.48
69:A5:2268:G:N2	69:A5:2469:U:O2	2.47	0.48
41:Ag:129:THR:OG1	41:Ag:130:ILE:N	2.47	0.48
52:AA:85:ARG:NE	52:AA:203:PHE:O	2.42	0.48
63:AC:49:LEU:HA	63:AC:52:LEU:HD13	1.94	0.48
64:AG:132:ARG:HE	64:AG:133:LEU:HG	1.77	0.48
64:AG:132:ARG:HH22	70:B2:146:C:H1'	1.78	0.48
69:A5:555:U:H2'	69:A5:556:A:H8	1.78	0.48
69:A5:2830:G:N2	69:A5:2888:A:O2'	2.45	0.48
70:B2:562:C:N4	70:B2:579:G:O6	2.47	0.48
70:B2:1302:U:O5'	70:B2:1333:C:O2'	2.29	0.48
9:CQ:20:SER:OG	69:A5:823:U:OP1	2.24	0.48
11:CA:249:GLY:HA2	70:B2:1074:G:C6	2.48	0.48
12:CS:175:TYR:CD2	12:CS:176:PHE:HA	2.49	0.48
14:CP:52:ILE:HG23	14:CP:85:LYS:HG3	1.95	0.48
17:CZ:72:LEU:O	17:CZ:106:ARG:NH2	2.46	0.48
21:CB:230:GLY:O	21:CB:234:ARG:NH1	2.46	0.48
45:AM:55:VAL:HA	45:AM:136:ARG:HH22	1.79	0.48
50:AP:88:ILE:HB	50:AP:92:MET:HE1	1.95	0.48
54:AY:22:LYS:HB2	54:AY:76:ILE:HB	1.96	0.48
57:Ab:30:SER:HB2	57:Ab:49:HIS:HD2	1.77	0.48
60:Af:78:LYS:HE2	70:B2:1637:G:H21	1.78	0.48
62:AE:182:MET:HG3	62:AE:192:VAL:HG22	1.95	0.48
64:AG:102:VAL:HG11	64:AG:109:LEU:HD21	1.95	0.48
65:AH:112:GLN:NE2	70:B2:901:G:N3	2.60	0.48
69:A5:659:U:H2'	69:A5:660:A:C8	2.49	0.48
69:A5:1711:C:H2'	69:A5:1712:C:C2	2.49	0.48
69:A5:3420:U:H5'	69:A5:3468:G:H21	1.79	0.48
70:B2:1452:U:O2	70:B2:1534:G:N2	2.46	0.48
2:CL:61:PRO:HG3	69:A5:79:G:H1'	1.94	0.48
10:CR:47:ASP:OD1	10:CR:47:ASP:N	2.32	0.48
25:Cf:50:LEU:HB2	69:A5:3714:U:H5	1.78	0.48
25:Cf:51:PHE:HA	25:Cf:149:ARG:HB3	1.94	0.48
35:CH:112:ILE:HG23	35:CH:122:ARG:HB2	1.95	0.48
41:Ag:245:ASN:OD1	41:Ag:246:ARG:N	2.46	0.48
42:AU:27:THR:HA	42:AU:88:LYS:HB3	1.96	0.48
58:AD:62:GLY:HA3	58:AD:67:ARG:HB2	1.94	0.48
60:Af:83:LYS:NZ	70:B2:1297:C:O3'	2.47	0.48
60:Af:145:ASN:OD1	60:Af:145:ASN:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:AG:58:LYS:HA	64:AG:59:GLN:HA	1.66	0.48
65:AH:67:GLN:O	65:AH:71:GLN:OE1	2.32	0.48
67:AQ:135:GLY:N	70:B2:1796:C:OP1	2.46	0.48
69:A5:371:G:O6	77:Cj:55:ARG:NH1	2.46	0.48
69:A5:3185:C:O2'	69:A5:3189:A:N1	2.40	0.48
70:B2:450:A:H1'	70:B2:533:A:H5'	1.96	0.48
70:B2:1695:A:N3	81:AS:82:TRP:HZ2	2.00	0.48
81:AS:27:GLY:HA2	81:AS:42:ASN:HD21	1.77	0.48
1:CO:115:ASP:OD1	1:CO:115:ASP:N	2.46	0.48
3:CV:90:ARG:NE	3:CV:124:GLU:OE2	2.47	0.48
7:CI:61:SER:HA	7:CI:126:VAL:HG23	1.95	0.48
8:CD:189:SER:O	8:CD:189:SER:OG	2.30	0.48
8:CD:206:ASP:OD1	8:CD:209:ARG:NH2	2.46	0.48
19:Ch:52:LYS:NZ	40:A8:62:A:O2'	2.46	0.48
25:Cf:51:PHE:CG	25:Cf:149:ARG:HG2	2.49	0.48
49:AR:90:ALA:HA	52:AA:20:VAL:HG21	1.95	0.48
57:Ab:61:THR:OG1	57:Ab:62:ILE:N	2.41	0.48
62:AE:136:VAL:HG23	62:AE:137:PRO:HD3	1.95	0.48
67:AQ:117:TYR:HB3	67:AQ:119:ARG:HE	1.78	0.48
69:A5:94:C:O2'	69:A5:300:A:OP1	2.31	0.48
70:B2:1736:U:O5'	81:AS:131:VAL:CG2	2.61	0.48
72:AT:63:HIS:O	72:AT:68:SER:N	2.45	0.48
80:Cd:56:THR:HG1	80:Cd:101:THR:HG1	1.60	0.48
12:CS:173:ARG:HH22	69:A5:3731:U:H5'	1.78	0.48
21:CB:242:ARG:HG3	69:A5:2714:U:H5''	1.95	0.48
21:CB:260:SER:O	21:CB:260:SER:OG	2.26	0.48
24:Ce:71:THR:HG23	24:Ce:73:PHE:HD1	1.78	0.48
41:Ag:31:ILE:H	41:Ag:43:TRP:HB2	1.79	0.48
69:A5:872:A:H1'	69:A5:873:U:H5''	1.95	0.48
69:A5:1021:U:H2'	69:A5:1022:A:C8	2.48	0.48
12:CS:173:ARG:HB3	12:CS:175:TYR:CE1	2.49	0.48
24:Ce:104:SER:OG	24:Ce:127:ARG:O	2.23	0.48
34:CJ:34:SER:OG	34:CJ:35:GLY:N	2.46	0.48
34:CJ:80:ARG:NE	39:A7:40:C:O2	2.35	0.48
37:CG:154:GLN:HB2	37:CG:156:LYS:HG3	1.96	0.48
46:Ad:44:ARG:NH1	70:B2:1367:C:OP1	2.46	0.48
51:AB:217:LYS:NZ	70:B2:973:U:OP1	2.47	0.48
61:AJ:168:GLY:HA2	61:AJ:171:PRO:HB3	1.94	0.48
64:AG:99:GLY:O	64:AG:101:ILE:N	2.46	0.48
65:AH:18:PHE:O	65:AH:21:SER:OG	2.28	0.48
66:AI:12:ARG:HB3	66:AI:18:ARG:HH21	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:Cz:91:LYS:HD3	68:Cz:94:ASN:HB2	1.95	0.48
69:A5:884:U:H3'	69:A5:885:U:H6	1.79	0.48
69:A5:1434:U:O2'	69:A5:1501:A:N1	2.42	0.48
69:A5:1986:G:H1	69:A5:2086:U:H3	1.62	0.48
69:A5:2640:A:O2'	70:B2:1975:G:N3	2.43	0.48
70:B2:1736:U:C5'	81:AS:131:VAL:CG2	2.74	0.48
71:AW:79:PHE:HB2	71:AW:125:ILE:HD12	1.95	0.48
2:CL:16:TRP:HE3	2:CL:19:ARG:HH12	1.61	0.48
5:Ca:104:LEU:HB3	5:Ca:109:TYR:HB2	1.95	0.48
7:CI:55:ASP:OD1	7:CI:55:ASP:N	2.39	0.48
12:CS:163:ASN:HB3	12:CS:165:LYS:N	2.26	0.48
18:Cr:43:ARG:NE	18:Cr:48:VAL:HG13	2.28	0.48
21:CB:303:ALA:HA	21:CB:368:ILE:HD12	1.95	0.48
25:Cf:29:ALA:HB3	25:Cf:35:SER:HA	1.96	0.48
37:CG:61:ARG:NH2	69:A5:2917:A:O5'	2.45	0.48
41:Ag:9:GLY:HA3	41:Ag:51:THR:HA	1.96	0.48
44:AX:67:ARG:HG2	44:AX:115:ILE:HG12	1.96	0.48
45:AM:76:CYS:O	45:AM:78:GLU:N	2.46	0.48
50:AP:21:ARG:CB	81:AS:93:GLY:HA2	2.31	0.48
63:AC:100:ARG:NE	70:B2:1235:A:OP1	2.41	0.48
69:A5:30:A:H4'	69:A5:347:A:C8	2.49	0.48
69:A5:1911:C:O2'	69:A5:1927:U:OP2	2.24	0.48
69:A5:2215:G:O2'	69:A5:2712:U:O4	2.26	0.48
69:A5:2909:A:N6	69:A5:3124:G:O2'	2.42	0.48
70:B2:1757:G:OP1	72:AT:38:LYS:NZ	2.43	0.48
8:CD:50:ARG:HG3	8:CD:52:ILE:HD11	1.96	0.47
9:CQ:124:ASP:OD1	9:CQ:124:ASP:N	2.46	0.47
9:CQ:131:PRO:HB2	29:CC:304:VAL:HG21	1.96	0.47
18:Cr:42:TYR:N	69:A5:1594:U:OP1	2.47	0.47
37:CG:89:SER:HA	37:CG:91:THR:HG23	1.96	0.47
42:AU:34:LEU:HA	42:AU:37:VAL:HG22	1.96	0.47
51:AB:131:LYS:HD3	51:AB:135:GLY:HA2	1.95	0.47
57:Ab:26:GLN:NE2	70:B2:950:U:OP2	2.43	0.47
67:AQ:36:VAL:N	67:AQ:39:ARG:O	2.47	0.47
68:Cz:166:SER:O	69:A5:2843:G:O2'	2.31	0.47
69:A5:178:U:H2'	69:A5:179:C:H6	1.79	0.47
69:A5:3463:U:H2'	69:A5:3464:G:O4'	2.14	0.47
70:B2:58:U:O2	70:B2:456:A:O2'	2.31	0.47
70:B2:720:G:N2	70:B2:783:U:OP2	2.45	0.47
70:B2:1590:G:OP1	70:B2:1595:G:N2	2.47	0.47
5:Ca:4:ILE:HB	69:A5:1671:U:O4	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Cr:47:ILE:HG23	18:Cr:49:HIS:H	1.79	0.47
37:CG:180:ARG:HG3	37:CG:235:HIS:CG	2.48	0.47
55:AZ:61:VAL:O	55:AZ:64:TYR:N	2.46	0.47
63:AC:157:ILE:O	63:AC:183:ARG:NH2	2.46	0.47
69:A5:593:U:O4	69:A5:615:C:N4	2.45	0.47
69:A5:864:G:O2'	69:A5:920:G:O2'	2.23	0.47
69:A5:1712:C:C6	69:A5:1713:U:H5'	2.49	0.47
70:B2:1447:G:OP1	70:B2:1538:C:N4	2.36	0.47
4:CM:11:ARG:NH2	4:CM:58:THR:O	2.48	0.47
11:CA:117:GLU:HB2	11:CA:162:ASN:HB2	1.96	0.47
22:CF:52:GLU:O	22:CF:56:ARG:N	2.40	0.47
34:CJ:104:PHE:HB3	34:CJ:164:LYS:HG3	1.95	0.47
34:CJ:161:ARG:NH1	69:A5:3218:C:OP1	2.42	0.47
41:Ag:48:ASP:OD1	41:Ag:48:ASP:N	2.47	0.47
52:AA:158:ASP:OD1	52:AA:158:ASP:N	2.45	0.47
58:AD:96:ARG:NH2	58:AD:127:TYR:OH	2.46	0.47
61:AJ:96:ASP:OD2	63:AC:183:ARG:NH1	2.47	0.47
63:AC:162:THR:HG22	63:AC:204:ASP:H	1.79	0.47
69:A5:401:G:N2	69:A5:404:U:OP2	2.40	0.47
69:A5:593:U:N3	69:A5:616:A:N1	2.61	0.47
2:CL:79:GLU:OE2	2:CL:103:ASN:ND2	2.47	0.47
2:CL:198:ARG:HA	2:CL:201:GLU:HG2	1.96	0.47
21:CB:268:ARG:HH12	69:A5:2770:C:HO2'	1.61	0.47
36:CE:171:LEU:HD22	36:CE:172:LYS:HG3	1.96	0.47
45:AM:72:VAL:HA	45:AM:75:LEU:HD12	1.96	0.47
69:A5:198:A:H5''	69:A5:199:U:H5	1.79	0.47
69:A5:2266:U:H3	69:A5:2475:A:N6	2.13	0.47
70:B2:444:U:O4'	70:B2:470:G:N2	2.48	0.47
70:B2:1758:A:C1'	81:AS:85:ASN:HD21	2.28	0.47
6:CN:19:MET:HE3	6:CN:19:MET:HB3	1.68	0.47
7:CI:181:TYR:HE1	7:CI:197:VAL:HG11	1.79	0.47
9:CQ:38:ARG:NH1	69:A5:1563:A:OP1	2.47	0.47
20:Cb:42:ASN:C	20:Cb:45:TYR:H	2.23	0.47
29:CC:10:VAL:N	29:CC:25:ILE:O	2.45	0.47
42:AU:106:ILE:HA	42:AU:107:ASN:HA	1.64	0.47
47:AN:70:LYS:NZ	70:B2:1050:A:N7	2.62	0.47
49:AR:95:ILE:HG12	52:AA:19:LEU:HD23	1.97	0.47
50:AP:100:TYR:OH	70:B2:1299:A:N3	2.40	0.47
52:AA:76:VAL:HG12	52:AA:123:VAL:HB	1.96	0.47
63:AC:215:THR:O	63:AC:215:THR:OG1	2.32	0.47
69:A5:441:A:C2	69:A5:2741:A:H4'	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:A5:1784:A:H2	69:A5:1785:G:C8	2.32	0.47
69:A5:1799:U:H5''	69:A5:1800:U:C5	2.49	0.47
69:A5:2170:C:O2	79:Cg:13:TYR:OH	2.30	0.47
70:B2:345:U:H2'	70:B2:346:A:C8	2.49	0.47
70:B2:1674:C:H41	70:B2:1716:A:H5''	1.78	0.47
74:AF:58:ASP:O	74:AF:61:LEU:N	2.47	0.47
75:Ac:33:GLU:OE2	75:Ac:36:ARG:NH2	2.47	0.47
77:Cj:39:TYR:O	77:Cj:41:ALA:N	2.47	0.47
3:CV:22:VAL:HA	3:CV:23:GLY:HA2	1.74	0.47
5:Ca:4:ILE:O	5:Ca:10:ARG:HG3	2.15	0.47
7:CI:22:PHE:HB3	69:A5:1261:A:C6	2.48	0.47
7:CI:157:PHE:O	69:A5:3385:G:N2	2.39	0.47
9:CQ:7:HIS:CE1	9:CQ:8:LYS:HB2	2.50	0.47
10:CR:15:LEU:HB3	10:CR:52:LYS:HG3	1.96	0.47
11:CA:244:GLY:HA3	69:A5:2620:C:H5''	1.96	0.47
16:CY:122:ARG:HG2	69:A5:200:U:H5''	1.96	0.47
25:Cf:138:ASN:HB2	69:A5:448:A:H4'	1.96	0.47
29:CC:34:PRO:O	29:CC:129:SER:OG	2.27	0.47
40:A8:8:A:H2'	40:A8:9:G:C8	2.45	0.47
41:Ag:143:ILE:HG22	41:Ag:145:GLU:H	1.79	0.47
41:Ag:143:ILE:HD11	41:Ag:180:LEU:HD11	1.95	0.47
42:AU:30:ASN:ND2	42:AU:109:GLU:OE2	2.47	0.47
50:AP:82:HIS:H	70:B2:1328:G:H4'	1.78	0.47
54:AY:8:ILE:O	54:AY:9:ARG:NH2	2.41	0.47
54:AY:113:ASN:HD22	70:B2:54:C:H5''	1.79	0.47
56:Aa:23:CYS:SG	56:Aa:24:THR:N	2.87	0.47
57:Ab:14:GLU:OE1	57:Ab:17:ARG:NH2	2.47	0.47
66:AI:99:ASN:OD1	66:AI:99:ASN:N	2.48	0.47
67:AQ:93:ALA:O	67:AQ:97:PHE:N	2.47	0.47
69:A5:1193:A:O2'	69:A5:1194:A:OP1	2.32	0.47
70:B2:218:A:OP2	70:B2:916:U:O2'	2.32	0.47
70:B2:855:C:H1'	70:B2:871:G:H22	1.79	0.47
70:B2:1445:A:H4'	72:AT:129:ARG:HD2	1.95	0.47
2:CL:90:ALA:O	2:CL:95:ILE:N	2.46	0.47
4:CM:120:ASN:ND2	69:A5:3767:G:OP2	2.36	0.47
7:CI:10:ARG:NH2	7:CI:59:GLN:OE1	2.42	0.47
11:CA:1:MET:N	69:A5:2793:C:OP2	2.48	0.47
11:CA:65:ASP:OD2	11:CA:72:ARG:NE	2.36	0.47
13:CT:132:PRO:HB2	22:CF:129:ASN:HB2	1.96	0.47
14:CP:3:ARG:HE	69:A5:416:C:H5''	1.80	0.47
21:CB:87:VAL:HG22	21:CB:110:LEU:HD22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:CB:110:LEU:HB2	21:CB:115:ARG:HD3	1.96	0.47
26:CI:13:LYS:HD2	26:CI:15:HIS:CD2	2.49	0.47
41:AG:133:TRP:O	41:AG:140:LYS:NZ	2.47	0.47
41:AG:168:SER:O	41:AG:176:LYS:N	2.48	0.47
42:AU:38:CYS:SG	42:AU:39:ARG:N	2.87	0.47
44:AX:11:ARG:NH1	70:B2:639:G:O2'	2.48	0.47
45:AM:49:LEU:HD21	45:AM:117:VAL:HG11	1.97	0.47
56:Aa:107:ALA:H	56:Aa:108:ARG:HA	1.79	0.47
59:Ae:75:HIS:NE2	59:Ae:77:SER:O	2.47	0.47
59:Ae:80:ARG:NH2	70:B2:574:C:O2'	2.47	0.47
61:AJ:14:TYR:OH	61:AJ:46:ARG:NH2	2.36	0.47
69:A5:1017:A:N3	77:Cj:11:ARG:HB3	2.30	0.47
69:A5:1261:A:O2'	69:A5:3164:C:O2'	2.20	0.47
69:A5:1910:C:H4'	69:A5:1926:A:H62	1.79	0.47
69:A5:1911:C:O5'	69:A5:2128:A:N6	2.44	0.47
70:B2:143:U:H2'	70:B2:144:A:H8	1.79	0.47
73:AK:44:ILE:HA	73:AK:48:GLN:HB2	1.96	0.47
14:CP:153:LYS:HE2	14:CP:153:LYS:HB2	1.70	0.47
26:CI:41:ASN:OD1	26:CI:41:ASN:N	2.48	0.47
43:AO:34:TYR:HD1	43:AO:98:ARG:HE	1.62	0.47
43:AO:149:ARG:NH1	70:B2:1094:C:O3'	2.48	0.47
63:AC:162:THR:HA	63:AC:202:ILE:HG23	1.97	0.47
64:AG:58:LYS:NZ	64:AG:106:MET:O	2.48	0.47
65:AH:98:ILE:HG22	65:AH:123:VAL:HG11	1.96	0.47
69:A5:826:A:O2'	69:A5:986:A:N1	2.37	0.47
69:A5:3591:A:HO2'	69:A5:3620:G:H1	1.63	0.47
71:AW:66:THR:OG1	71:AW:67:GLY:N	2.47	0.47
73:AK:13:GLU:HA	73:AK:16:PHE:HB3	1.97	0.47
80:Cd:42:ALA:O	80:Cd:46:ILE:HG12	2.15	0.47
80:Cd:54:MET:O	80:Cd:87:ARG:NH1	2.48	0.47
7:CI:116:ARG:HH21	69:A5:3154:C:H42	1.62	0.47
10:CR:74:ARG:HD3	10:CR:74:ARG:HA	1.69	0.47
28:CI:26:TRP:CZ3	40:A8:49:C:H2'	2.50	0.47
39:A7:12:U:H4'	39:A7:67:G:H21	1.80	0.47
51:AB:49:VAL:HG21	51:AB:62:LEU:HD22	1.96	0.47
61:AJ:33:ILE:HD11	61:AJ:41:LYS:HD3	1.97	0.47
67:AQ:97:PHE:HA	67:AQ:100:LYS:HZ3	1.79	0.47
68:Cz:130:LYS:HG2	69:A5:2879:A:H5'	1.97	0.47
69:A5:3942:U:H4'	69:A5:3943:G:H5'	1.96	0.47
70:B2:1732:G:H1	70:B2:1763:C:H42	1.62	0.47
4:CM:33:GLN:NE2	69:A5:1400:A:OP1	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Ca:96:SER:HA	5:Ca:121:ARG:HH22	1.80	0.47
19:Ch:5:LYS:HB2	19:Ch:8:GLU:HG2	1.97	0.47
35:CH:105:GLU:HA	35:CH:106:ASN:HA	1.61	0.47
41:Ag:241:CYS:HB2	41:Ag:290:LEU:HB3	1.97	0.47
53:AV:17:CYS:SG	53:AV:18:SER:N	2.88	0.47
54:AY:28:VAL:O	54:AY:70:SER:N	2.46	0.47
55:AZ:99:VAL:HG21	74:AF:124:GLU:HG3	1.97	0.47
58:AD:64:LYS:HD2	58:AD:66:ARG:HH11	1.79	0.47
60:Af:140:TYR:HB3	60:Af:149:VAL:HG13	1.97	0.47
65:AH:142:ILE:HG12	71:AW:52:ILE:HB	1.96	0.47
68:Cz:7:ARG:NH2	68:Cz:13:GLY:O	2.48	0.47
70:B2:1906:U:H2'	70:B2:1907:G:H8	1.80	0.47
8:CD:37:THR:HA	8:CD:48:LYS:HD2	1.97	0.46
10:CR:45:ILE:HD13	10:CR:50:ILE:HB	1.97	0.46
25:Cf:4:THR:HG22	25:Cf:7:LYS:HB2	1.95	0.46
25:Cf:90:LYS:HA	25:Cf:154:PRO:HD2	1.97	0.46
29:CC:317:ARG:NH1	69:A5:551:C:O2'	2.46	0.46
36:CE:202:GLN:HA	36:CE:205:VAL:HG22	1.98	0.46
44:AX:107:ARG:HG3	44:AX:112:VAL:HG12	1.95	0.46
45:AM:28:VAL:HA	45:AM:125:THR:HG21	1.96	0.46
50:AP:114:MET:O	50:AP:117:HIS:ND1	2.48	0.46
55:AZ:81:SER:HG	81:AS:55:ARG:NH2	1.78	0.46
64:AG:39:ASP:HB2	64:AG:46:LYS:HD3	1.96	0.46
69:A5:892:A:H2'	69:A5:893:U:H4'	1.96	0.46
69:A5:1456:U:H1'	69:A5:1458:G:H5''	1.97	0.46
70:B2:252:A:O2'	70:B2:254:C:OP2	2.28	0.46
71:AW:5:ASN:HB3	71:AW:8:ALA:H	1.80	0.46
2:CL:26:ASN:OD1	2:CL:26:ASN:N	2.45	0.46
4:CM:155:LYS:HA	4:CM:156:ALA:HA	1.64	0.46
7:CI:65:LEU:HD21	7:CI:91:LEU:HD12	1.97	0.46
8:CD:51:LEU:HB2	8:CD:144:CYS:HB3	1.98	0.46
27:Ck:36:ILE:HG22	27:Ck:43:TYR:HB2	1.95	0.46
29:CC:81:ARG:HB3	29:CC:91:GLY:O	2.16	0.46
29:CC:339:LYS:HG2	69:A5:652:G:H3'	1.96	0.46
51:AB:124:ILE:HD11	51:AB:210:LEU:HD21	1.97	0.46
69:A5:889:G:H1	69:A5:899:G:H22	1.62	0.46
69:A5:1429:U:H2'	69:A5:1430:U:H6	1.80	0.46
77:Cj:68:LYS:HA	77:Cj:71:ARG:HG2	1.98	0.46
14:CP:104:CYS:SG	69:A5:399:C:O2'	2.64	0.46
18:Cr:32:GLU:OE2	18:Cr:35:ASN:ND2	2.49	0.46
50:AP:20:TYR:HA	81:AS:91:ILE:HD13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:AP:111:LYS:HB3	50:AP:114:MET:HE2	1.97	0.46
60:Af:111:ASN:HA	60:Af:112:GLY:HA2	1.64	0.46
65:AH:110:LEU:HG	65:AH:111:LYS:HG3	1.96	0.46
67:AQ:99:GLN:HE21	67:AQ:107:LYS:HD3	1.79	0.46
67:AQ:125:ASP:N	67:AQ:125:ASP:OD1	2.46	0.46
69:A5:1500:G:H4'	69:A5:1501:A:H8	1.80	0.46
69:A5:2833:U:H2'	69:A5:2878:A:H62	1.80	0.46
70:B2:1458:U:OP2	70:B2:1459:G:N1	2.44	0.46
72:AT:84:ARG:NH1	72:AT:85:ASN:O	2.48	0.46
73:AK:12:TYR:HD2	73:AK:81:LEU:HD11	1.79	0.46
18:Cr:109:ASP:HB2	69:A5:1565:A:H1'	1.97	0.46
22:CF:42:LYS:NZ	69:A5:1187:A:OP1	2.49	0.46
34:CJ:115:GLN:HA	34:CJ:132:GLY:HA2	1.96	0.46
41:Ag:42:VAL:HG13	41:Ag:57:GLN:HB3	1.97	0.46
41:Ag:49:GLU:HB3	41:Ag:52:ASN:HB3	1.98	0.46
67:AQ:132:LYS:NZ	70:B2:1797:G:OP2	2.38	0.46
68:Cz:51:GLY:HA3	68:Cz:193:LEU:HD21	1.96	0.46
69:A5:1207:G:O2'	69:A5:1266:A:N6	2.41	0.46
69:A5:3907:G:N7	78:CW:35:LYS:NZ	2.63	0.46
70:B2:1758:A:H5''	81:AS:36:VAL:HA	1.96	0.46
10:CR:113:LYS:HA	10:CR:113:LYS:HD2	1.72	0.46
10:CR:186:ALA:O	10:CR:190:LYS:N	2.48	0.46
17:CZ:9:LYS:NZ	17:CZ:83:THR:O	2.39	0.46
24:Ce:84:LEU:HD22	24:Ce:110:ILE:HG23	1.96	0.46
36:CE:101:LEU:HD11	36:CE:115:LEU:HG	1.98	0.46
46:Ad:48:ASN:HA	46:Ad:49:ASP:HA	1.60	0.46
52:AA:80:ARG:NH2	52:AA:165:ASN:O	2.48	0.46
55:AZ:82:LEU:HD23	55:AZ:85:ARG:HD2	1.96	0.46
66:AI:180:ARG:NH2	70:B2:336:A:N7	2.64	0.46
69:A5:328:U:O2	69:A5:3312:G:N2	2.49	0.46
69:A5:539:G:OP1	69:A5:540:G:O2'	2.33	0.46
69:A5:593:U:O4	69:A5:616:A:N6	2.48	0.46
69:A5:3124:G:H4'	69:A5:3126:C:C2	2.51	0.46
70:B2:720:G:H5''	70:B2:721:U:H5'	1.97	0.46
70:B2:1444:C:OP1	70:B2:1540:G:N2	2.49	0.46
70:B2:1600:A:H3'	70:B2:1601:A:C8	2.50	0.46
72:AT:27:LYS:HZ1	72:AT:106:ALA:H	1.63	0.46
9:CQ:107:GLN:OE1	9:CQ:111:GLU:OE2	2.34	0.46
14:CP:122:ALA:HB3	14:CP:143:PRO:HB2	1.98	0.46
24:Ce:79:HIS:N	24:Ce:83:GLU:OE1	2.43	0.46
29:CC:208:ARG:NH2	69:A5:1624:G:OP1	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Ag:215:SER:O	41:Ag:215:SER:OG	2.33	0.46
44:AX:86:PRO:HB2	44:AX:87:ARG:HG2	1.97	0.46
45:AM:99:CYS:HB3	45:AM:101:ILE:HB	1.97	0.46
48:AL:64:ARG:NH2	70:B2:254:C:O2'	2.48	0.46
50:AP:84:ARG:NH2	70:B2:1645:G:O2'	2.35	0.46
55:AZ:46:GLN:HG2	81:AS:23:LYS:CG	2.45	0.46
61:AJ:55:ARG:O	61:AJ:59:ARG:N	2.41	0.46
64:AG:48:TYR:OH	64:AG:119:LYS:O	2.28	0.46
68:Cz:175:LYS:HG2	68:Cz:178:GLU:HB2	1.97	0.46
69:A5:555:U:H2'	69:A5:556:A:C8	2.51	0.46
69:A5:765:A:H3'	69:A5:766:G:C8	2.51	0.46
70:B2:139:U:N3	70:B2:140:G:N7	2.64	0.46
74:AF:59:ILE:HA	74:AF:60:SER:HA	1.62	0.46
80:Cd:65:LEU:O	80:Cd:69:ILE:HG12	2.16	0.46
1:CO:118:ARG:NH2	69:A5:3721:C:H41	2.14	0.46
8:CD:53:VAL:HG13	8:CD:159:VAL:HG13	1.98	0.46
8:CD:277:GLN:O	8:CD:281:LYS:N	2.47	0.46
11:CA:252:ASP:OD1	11:CA:252:ASP:N	2.40	0.46
14:CP:64:ASN:O	14:CP:80:GLN:NE2	2.48	0.46
15:CX:177:ARG:HG3	15:CX:179:PRO:HD3	1.97	0.46
18:Cr:12:ILE:HD12	18:Cr:16:ASN:HD22	1.80	0.46
19:Ch:112:SER:HB2	69:A5:270:G:H21	1.80	0.46
23:Cc:31:TYR:OH	23:Cc:59:GLU:OE2	2.26	0.46
34:CJ:96:GLU:O	34:CJ:98:GLU:N	2.48	0.46
36:CE:237:TYR:HB3	36:CE:239:HIS:N	2.31	0.46
40:A8:46:C:H1'	40:A8:60:U:H2'	1.98	0.46
41:Ag:17:TRP:HB3	41:Ag:288:LEU:HD11	1.98	0.46
44:AX:91:LEU:HD22	59:Ae:78:LEU:HD21	1.98	0.46
51:AB:133:VAL:HG12	51:AB:183:ASP:H	1.80	0.46
54:AY:18:LEU:HD22	62:AE:95:THR:HG23	1.98	0.46
55:AZ:73:SER:HA	55:AZ:78:ILE:HG12	1.97	0.46
62:AE:19:MET:HB2	62:AE:51:ARG:HH22	1.81	0.46
67:AQ:84:TYR:O	67:AQ:87:ARG:NE	2.49	0.46
69:A5:2928:G:H1	69:A5:2990:C:H42	1.64	0.46
69:A5:3374:U:OP1	69:A5:3376:C:N4	2.49	0.46
76:CU:245:SER:OG	76:CU:246:ASP:N	2.48	0.46
3:CV:26:MET:HE2	3:CV:26:MET:HB3	1.82	0.46
16:CY:35:SER:HA	16:CY:105:LEU:HD11	1.97	0.46
22:CF:95:VAL:HG22	22:CF:145:TRP:HB3	1.98	0.46
24:Ce:37:PRO:HG2	24:Ce:45:ARG:HB2	1.97	0.46
29:CC:274:SER:OG	29:CC:275:THR:N	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:CJ:29:ILE:HG12	34:CJ:133:LEU:HG	1.98	0.46
36:CE:24:SER:HA	36:CE:27:LYS:HD3	1.97	0.46
40:A8:111:G:OP1	69:A5:2147:C:O2'	2.31	0.46
55:AZ:62:PRO:HA	55:AZ:63:ALA:HA	1.60	0.46
58:AD:179:LEU:HD13	58:AD:184:LEU:HB3	1.96	0.46
62:AE:94:LYS:HA	62:AE:95:THR:HA	1.67	0.46
67:AQ:47:LYS:HD3	67:AQ:50:GLN:HB2	1.98	0.46
69:A5:2843:G:H2'	69:A5:2844:G:C8	2.51	0.46
70:B2:1990:U:O2'	70:B2:1992:A:N7	2.41	0.46
4:CM:130:LEU:HG	4:CM:132:LYS:H	1.81	0.46
12:CS:9:GLU:HB3	12:CS:33:PHE:CE1	2.51	0.46
12:CS:30:MET:HG3	12:CS:44:PHE:CD1	2.50	0.46
21:CB:333:ILE:HA	21:CB:333:ILE:HD13	1.86	0.46
41:Ag:17:TRP:HB2	41:Ag:36:ARG:HD2	1.98	0.46
54:AY:103:GLN:HB3	54:AY:108:ARG:HB2	1.97	0.46
64:AG:64:LYS:HZ3	64:AG:81:HIS:HB3	1.81	0.46
64:AG:131:ARG:NH1	64:AG:133:LEU:O	2.49	0.46
67:AQ:1:MET:HA	70:B2:1564:A:H5''	1.97	0.46
67:AQ:28:LYS:HD2	70:B2:1438:U:H4'	1.96	0.46
67:AQ:74:VAL:HG11	67:AQ:82:GLN:HB3	1.97	0.46
69:A5:2845:G:N2	69:A5:2881:U:OP2	2.43	0.46
69:A5:3660:U:H2'	69:A5:3661:C:H6	1.80	0.46
70:B2:160:G:OP2	70:B2:160:G:N2	2.42	0.46
70:B2:650:G:N2	70:B2:710:C:O2	2.48	0.46
70:B2:834:A:H61	70:B2:882:G:H1	1.62	0.46
80:Cd:94:ASP:HB2	80:Cd:98:LYS:HE2	1.97	0.46
9:CQ:31:LEU:HD21	29:CC:295:LEU:HD13	1.98	0.46
13:CT:72:VAL:HG13	13:CT:93:ILE:HD11	1.98	0.46
17:CZ:6:LYS:HE3	17:CZ:6:LYS:HB2	1.83	0.46
17:CZ:36:LYS:NZ	17:CZ:74:SER:OG	2.39	0.46
33:Co:63:THR:OG1	69:A5:3184:U:OP1	2.33	0.46
34:CJ:49:THR:O	34:CJ:83:LYS:NZ	2.49	0.46
50:AP:117:HIS:HB3	50:AP:121:GLU:HG3	1.98	0.46
57:Ab:25:VAL:HG22	71:AW:55:ASP:HB3	1.97	0.46
63:AC:193:PRO:HA	63:AC:196:LEU:HB3	1.97	0.46
68:Cz:148:ILE:O	68:Cz:152:LYS:N	2.46	0.46
70:B2:1259:A:H2'	70:B2:1260:G:C8	2.51	0.46
18:Cr:116:ARG:HB3	36:CE:75:VAL:HG12	1.98	0.45
20:Cb:41:ILE:HG22	69:A5:1289:C:H1'	1.98	0.45
39:A7:67:G:H1	39:A7:108:G:H1	1.64	0.45
41:Ag:81:SER:OG	41:Ag:89:ARG:N	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:AX:29:LYS:HG2	44:AX:35:ARG:HH21	1.80	0.45
48:AL:133:LYS:HB2	70:B2:342:G:H3'	1.98	0.45
50:AP:17:LYS:HD2	50:AP:17:LYS:HA	1.78	0.45
62:AE:141:THR:OG1	62:AE:145:ARG:O	2.30	0.45
64:AG:75:LEU:HD11	70:B2:1917:A:H5''	1.97	0.45
68:Cz:34:LEU:N	68:Cz:167:VAL:O	2.42	0.45
69:A5:546:G:N2	69:A5:756:C:N3	2.46	0.45
69:A5:1507:C:H2'	69:A5:1508:U:H6	1.81	0.45
69:A5:2072:C:H42	69:A5:2080:G:H1	1.64	0.45
70:B2:618:G:HO2'	70:B2:621:G:HO2'	1.44	0.45
77:Cj:54:LYS:O	77:Cj:58:THR:OG1	2.32	0.45
79:Cg:42:PRO:HB2	79:Cg:51:LEU:HD12	1.97	0.45
81:AS:34:LYS:O	81:AS:100:SER:OG	2.32	0.45
1:CO:201:TYR:CD1	4:CM:101:ARG:HG2	2.51	0.45
3:CV:13:LYS:O	69:A5:3575:G:O2'	2.34	0.45
6:CN:187:SER:H	6:CN:190:ALA:HB3	1.81	0.45
7:CI:210:GLU:O	7:CI:214:ARG:N	2.44	0.45
8:CD:104:LEU:HD13	8:CD:247:ILE:HG23	1.98	0.45
16:CY:87:ARG:HB3	16:CY:95:VAL:HG23	1.99	0.45
17:CZ:14:LEU:HD11	17:CZ:81:MET:HB2	1.97	0.45
21:CB:48:GLY:HA2	21:CB:81:THR:HG22	1.98	0.45
29:CC:123:ARG:HH11	29:CC:123:ARG:HD2	1.59	0.45
33:Co:64:LYS:HG2	69:A5:3325:G:H5''	1.98	0.45
34:CJ:116:GLU:HG2	34:CJ:130:ILE:HD11	1.97	0.45
35:CH:23:ARG:HH11	35:CH:39:LYS:HA	1.81	0.45
36:CE:105:ALA:HB1	69:A5:3844:U:C5	2.51	0.45
47:AN:3:ARG:HD3	47:AN:3:ARG:HA	1.78	0.45
58:AD:37:SER:HB3	58:AD:53:MET:HG3	1.98	0.45
62:AE:250:GLU:O	62:AE:254:LYS:N	2.47	0.45
67:AQ:35:LYS:NZ	70:B2:1540:G:OP1	2.48	0.45
69:A5:474:A:H62	69:A5:523:C:HO2'	1.59	0.45
69:A5:1566:U:H4'	69:A5:1567:G:H4'	1.99	0.45
69:A5:1583:G:H2'	69:A5:1584:A:H8	1.81	0.45
69:A5:1882:G:HO2'	69:A5:2066:G:HO2'	1.60	0.45
69:A5:2537:A:H4'	69:A5:2538:U:H5''	1.97	0.45
69:A5:3540:G:H21	69:A5:3675:A:H62	1.63	0.45
70:B2:1220:A:H2'	70:B2:1221:A:C8	2.51	0.45
70:B2:1468:G:H22	70:B2:1522:G:H1	1.63	0.45
70:B2:1707:A:O2'	70:B2:1709:A:OP2	2.34	0.45
26:CI:77:LYS:NZ	69:A5:2599:G:O6	2.48	0.45
31:Cn:11:ARG:NH2	70:B2:1215:G:OP1	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:CE:237:TYR:CE2	36:CE:240:ARG:HB3	2.52	0.45
37:CG:145:THR:O	37:CG:149:THR:OG1	2.33	0.45
43:AO:125:LYS:HE3	56:Aa:58:ILE:HG13	1.97	0.45
44:AX:3:LYS:NZ	70:B2:622:C:OP2	2.44	0.45
51:AB:70:SER:HA	51:AB:86:LYS:HA	1.97	0.45
54:AY:59:PHE:O	54:AY:91:ARG:NH2	2.40	0.45
58:AD:104:ALA:HB1	58:AD:175:ARG:HG2	1.97	0.45
58:AD:116:ALA:HB1	58:AD:119:ARG:HB3	1.99	0.45
64:AG:44:GLU:HB3	64:AG:119:LYS:HD3	1.99	0.45
67:AQ:15:PHE:N	67:AQ:92:LYS:HD3	2.30	0.45
68:Cz:17:LEU:HD13	68:Cz:179:LEU:HB2	1.99	0.45
69:A5:1963:U:H2'	69:A5:1964:A:C8	2.51	0.45
70:B2:439:G:N1	70:B2:442:A:OP2	2.45	0.45
70:B2:1027:A:N1	70:B2:1062:C:O2'	2.50	0.45
70:B2:1444:C:OP1	72:AT:129:ARG:NH1	2.49	0.45
70:B2:1582:C:H2'	70:B2:1583:A:H4'	1.99	0.45
72:AT:87:VAL:O	72:AT:88:HIS:ND1	2.49	0.45
74:AF:149:GLU:OE1	75:Ac:55:LEU:N	2.46	0.45
17:CZ:4:ILE:HG22	23:Cc:39:ARG:HA	1.98	0.45
22:CF:197:GLU:HG2	22:CF:202:GLY:HA3	1.98	0.45
33:Co:32:ARG:NE	69:A5:3299:U:OP1	2.48	0.45
36:CE:23:ASN:HB3	36:CE:32:ARG:HH22	1.80	0.45
39:A7:3:C:H2'	39:A7:4:A:C8	2.51	0.45
43:AO:141:ARG:O	70:B2:1076:U:O2'	2.33	0.45
64:AG:47:GLY:HA3	64:AG:117:GLY:HA3	1.98	0.45
64:AG:59:GLN:H	64:AG:72:ARG:HH21	1.65	0.45
64:AG:212:LYS:HA	64:AG:215:VAL:HG12	1.97	0.45
68:Cz:24:LYS:HE2	68:Cz:26:ARG:HB3	1.97	0.45
69:A5:1407:C:O2'	69:A5:1408:A:OP1	2.31	0.45
72:AT:21:PHE:HB3	72:AT:24:LYS:HE3	1.98	0.45
6:CN:158:HIS:CG	6:CN:161:LEU:HD12	2.51	0.45
7:CI:19:LYS:HA	7:CI:26:VAL:HG11	1.97	0.45
7:CI:50:VAL:HG22	7:CI:167:VAL:HA	1.98	0.45
8:CD:125:VAL:HG11	8:CD:199:ILE:HG21	1.99	0.45
10:CR:36:ASN:OD1	10:CR:36:ASN:N	2.50	0.45
18:Cr:62:LYS:HB3	18:Cr:125:GLN:HB2	1.97	0.45
21:CB:181:MET:HE2	21:CB:183:ILE:HG12	1.98	0.45
49:AR:10:LYS:HA	49:AR:13:ALA:HB3	1.98	0.45
49:AR:78:ARG:HH22	52:AA:201:LEU:HD11	1.82	0.45
53:AV:80:SER:OG	53:AV:81:LYS:N	2.49	0.45
57:Ab:19:HIS:HB3	57:Ab:22:LYS:H	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:AJ:19:ARG:NH2	70:B2:3:U:O2'	2.50	0.45
62:AE:127:LYS:HB3	62:AE:140:VAL:HG13	1.98	0.45
69:A5:705:G:H1	69:A5:732:U:H3	1.63	0.45
69:A5:1315:A:H5'	69:A5:1316:U:H5'	1.99	0.45
69:A5:1734:G:O2'	69:A5:2159:C:O2'	2.30	0.45
7:CI:98:ARG:HA	7:CI:122:PRO:HA	1.98	0.45
12:CS:17:LEU:HD23	12:CS:60:GLU:HG3	1.99	0.45
15:CX:266:ASP:OD1	15:CX:266:ASP:N	2.50	0.45
61:AJ:126:HIS:HB2	70:B2:484:C:H5'	1.99	0.45
62:AE:21:ASP:OD1	62:AE:21:ASP:N	2.38	0.45
63:AC:149:ARG:HB3	63:AC:230:THR:HB	1.98	0.45
65:AH:81:LEU:HB3	65:AH:90:VAL:HG11	1.98	0.45
70:B2:104:A:H62	70:B2:313:C:H5	1.64	0.45
70:B2:488:A:N6	70:B2:511:G:O6	2.49	0.45
70:B2:650:G:H1	70:B2:709:G:H22	1.63	0.45
70:B2:1760:G:N7	81:AS:38:ARG:NH2	2.65	0.45
2:CL:73:ARG:HD3	69:A5:80:G:H3'	1.97	0.45
11:CA:98:ILE:HA	11:CA:99:GLY:HA2	1.75	0.45
11:CA:131:GLY:H	11:CA:169:VAL:HG23	1.81	0.45
12:CS:174:THR:HB	69:A5:3729:A:H61	1.82	0.45
14:CP:75:GLN:HE22	69:A5:3966:U:H1'	1.82	0.45
18:Cr:69:LYS:O	18:Cr:71:GLY:N	2.42	0.45
25:Cf:46:ARG:N	25:Cf:76:GLU:OE1	2.50	0.45
25:Cf:86:PHE:O	25:Cf:90:LYS:NZ	2.47	0.45
35:CH:150:GLU:OE2	69:A5:3658:G:N2	2.37	0.45
41:Ag:214:ASP:OD1	41:Ag:214:ASP:N	2.45	0.45
42:AU:85:ARG:NH1	70:B2:1422:A:OP1	2.50	0.45
48:AL:106:MET:HE1	70:B2:310:C:H5''	1.99	0.45
52:AA:154:LEU:HG	52:AA:157:ILE:HD11	1.98	0.45
55:AZ:43:LEU:HD11	55:AZ:78:ILE:H	1.82	0.45
58:AD:7:ILE:HB	58:AD:12:LYS:HE3	1.99	0.45
61:AJ:176:ARG:HE	61:AJ:180:LYS:HE3	1.81	0.45
62:AE:79:ASP:HB3	62:AE:82:TYR:HB2	1.98	0.45
65:AH:115:PRO:HD3	70:B2:896:A:H62	1.81	0.45
67:AQ:111:LYS:O	67:AQ:115:VAL:N	2.50	0.45
67:AQ:137:PRO:HD3	67:AQ:143:TYR:HD1	1.80	0.45
69:A5:231:A:O2'	69:A5:233:A:OP2	2.30	0.45
69:A5:2822:C:H42	69:A5:2896:U:H3	1.64	0.45
69:A5:3719:A:H1'	69:A5:3764:G:H8	1.82	0.45
70:B2:1463:C:N4	70:B2:1524:A:OP2	2.50	0.45
71:AW:111:MET:HE2	71:AW:111:MET:HB3	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:CU:215:ILE:HG21	76:CU:241:LEU:HD21	1.98	0.45
80:Cd:20:ARG:NH1	80:Cd:54:MET:SD	2.90	0.45
3:CV:67:LYS:HA	3:CV:73:ARG:HH21	1.81	0.45
9:CQ:79:THR:HG23	9:CQ:99:THR:HB	1.98	0.45
17:CZ:59:LYS:N	69:A5:3104:C:OP2	2.50	0.45
18:Cr:69:LYS:HG3	18:Cr:70:LYS:HB2	1.98	0.45
21:CB:338:ILE:H	21:CB:338:ILE:HG13	1.54	0.45
27:Ck:19:ASP:OD1	27:Ck:19:ASP:N	2.40	0.45
27:Ck:24:LYS:HG3	27:Ck:35:LYS:HB2	1.98	0.45
35:CH:187:LYS:HA	35:CH:188:LEU:HA	1.67	0.45
37:CG:108:ARG:NH2	37:CG:197:ARG:O	2.50	0.45
39:A7:55:A:H3'	39:A7:56:G:C8	2.51	0.45
42:AU:30:ASN:HD22	42:AU:33:SER:HB2	1.82	0.45
52:AA:208:GLU:HA	52:AA:209:GLU:HA	1.56	0.45
63:AC:87:ASP:OD1	63:AC:87:ASP:N	2.50	0.45
68:Cz:6:SER:HB3	68:Cz:212:PRO:HG2	1.98	0.45
69:A5:3587:U:H2'	69:A5:3588:G:H8	1.82	0.45
70:B2:1728:G:OP1	74:AF:191:ASN:ND2	2.49	0.45
2:CL:62:THR:HG21	5:Ca:67:GLN:HE22	1.81	0.45
2:CL:140:LEU:HA	2:CL:142:GLU:HG2	1.99	0.45
4:CM:147:ARG:NH2	69:A5:3822:C:N3	2.64	0.45
7:CI:90:ARG:NH2	69:A5:1257:U:OP1	2.42	0.45
21:CB:24:ARG:H	21:CB:24:ARG:HG2	1.55	0.45
24:Ce:7:TYR:CZ	36:CE:77:LYS:HB3	2.52	0.45
47:AN:54:LEU:HB3	47:AN:60:VAL:HG12	1.98	0.45
48:AL:45:ARG:NH2	70:B2:932:U:O3'	2.50	0.45
50:AP:92:MET:HE2	50:AP:92:MET:HB3	1.88	0.45
51:AB:55:GLN:HG2	51:AB:56:ARG:HD3	1.99	0.45
52:AA:191:ARG:NH2	52:AA:192:SER:OG	2.50	0.45
55:AZ:97:LYS:O	55:AZ:109:THR:N	2.44	0.45
61:AJ:23:LYS:HA	61:AJ:26:LEU:HB3	1.99	0.45
61:AJ:170:ARG:NH2	70:B2:542:A:O3'	2.50	0.45
62:AE:254:LYS:HB2	62:AE:254:LYS:HE3	1.77	0.45
65:AH:114:ARG:NH2	70:B2:647:U:OP1	2.50	0.45
69:A5:1144:C:H2'	69:A5:1145:C:H6	1.82	0.45
69:A5:1951:C:H5''	79:Cg:72:VAL:HG13	1.99	0.45
69:A5:2933:A:O5'	69:A5:2986:G:N2	2.49	0.45
69:A5:3595:U:H2'	69:A5:3596:A:H8	1.82	0.45
70:B2:1087:C:H1'	70:B2:1090:A:H2	1.82	0.45
79:Cg:23:VAL:CG2	79:Cg:33:GLN:HB2	2.46	0.45
18:Cr:79:LYS:HG2	18:Cr:84:VAL:HG11	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Cr:112:GLN:H	18:Cr:112:GLN:HG2	1.46	0.45
20:Cb:62:GLU:HA	20:Cb:65:ALA:HB3	1.98	0.45
21:CB:293:THR:HA	21:CB:297:LYS:HA	2.00	0.45
26:Ci:10:GLY:O	26:Ci:12:ASN:ND2	2.50	0.45
47:AN:75:MET:O	47:AN:79:GLY:N	2.48	0.45
50:AP:80:LYS:HD3	50:AP:105:PHE:CG	2.52	0.45
51:AB:40:GLN:HB3	51:AB:41:THR:H	1.67	0.45
51:AB:117:VAL:HG22	51:AB:145:PHE:HZ	1.82	0.45
53:AV:7:GLU:HB3	53:AV:9:VAL:HG13	1.98	0.45
58:AD:44:THR:OG1	58:AD:47:ARG:O	2.29	0.45
64:AG:226:GLU:O	64:AG:230:ARG:N	2.49	0.45
65:AH:8:ILE:HG22	65:AH:44:ILE:H	1.82	0.45
68:Cz:2:ALA:O	68:Cz:4:LYS:NZ	2.49	0.45
69:A5:1911:C:OP1	69:A5:1924:A:O2'	2.27	0.45
70:B2:1259:A:H2'	70:B2:1260:G:H8	1.82	0.45
70:B2:1276:G:H2'	70:B2:1277:A:H8	1.81	0.45
70:B2:1750:U:H4'	81:AS:133:GLY:HA3	1.98	0.45
73:AK:54:GLY:HA2	73:AK:55:LEU:HB3	1.99	0.45
73:AK:58:GLU:HG3	73:AK:60:PHE:HD1	1.82	0.45
76:CU:255:LYS:HG2	76:CU:259:LYS:HE3	1.98	0.45
81:AS:25:LYS:HA	81:AS:55:ARG:HA	1.98	0.45
5:Ca:100:PRO:HD2	5:Ca:123:VAL:HA	1.97	0.44
8:CD:94:ASN:HB3	8:CD:96:ALA:H	1.81	0.44
8:CD:215:ASP:N	8:CD:215:ASP:OD1	2.50	0.44
9:CQ:64:GLN:HG3	9:CQ:92:LEU:HD13	1.98	0.44
13:CT:130:ARG:O	69:A5:1311:U:O2'	2.33	0.44
16:CY:100:HIS:CD2	69:A5:239:U:H4'	2.52	0.44
25:Cf:46:ARG:HB2	25:Cf:47:HIS:H	1.53	0.44
34:CJ:118:ILE:HG21	34:CJ:124:TYR:HA	1.99	0.44
66:AI:119:LEU:HD21	66:AI:155:GLN:HG3	1.98	0.44
66:AI:179:SER:OG	66:AI:180:ARG:N	2.50	0.44
67:AQ:8:PRO:O	67:AQ:28:LYS:NZ	2.41	0.44
69:A5:992:U:H2'	69:A5:993:A:C8	2.52	0.44
8:CD:245:GLN:HA	8:CD:248:ARG:HB2	1.99	0.44
8:CD:258:LYS:HG2	8:CD:261:SER:HB2	1.99	0.44
9:CQ:12:LYS:HG3	69:A5:1558:A:H5''	1.99	0.44
25:Cf:101:LYS:HB2	25:Cf:103:CYS:H	1.81	0.44
30:Cm:78:ILE:HB	30:Cm:83:ARG:HH21	1.82	0.44
43:AO:134:PRO:HB2	70:B2:974:A:H5'	1.99	0.44
50:AP:29:LEU:HD12	50:AP:30:ASP:HB2	1.98	0.44
55:AZ:51:LYS:HE3	81:AS:6:PRO:HG2	1.75	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:AZ:79:ARG:CZ	81:AS:23:LYS:HZ2	2.29	0.44
63:AC:51:ARG:O	63:AC:55:GLU:N	2.45	0.44
69:A5:2839:A:N6	69:A5:2880:A:O4'	2.49	0.44
70:B2:842:A:H2	70:B2:874:U:H3	1.65	0.44
80:Cd:84:ARG:NH1	80:Cd:120:GLU:OE1	2.50	0.44
2:CL:168:GLU:OE2	5:Ca:98:LYS:NZ	2.34	0.44
5:Ca:74:ILE:HD11	5:Ca:78:LYS:HB2	1.98	0.44
11:CA:156:LYS:NZ	11:CA:157:VAL:O	2.50	0.44
21:CB:200:HIS:HD2	21:CB:205:ILE:HD11	1.83	0.44
36:CE:97:PRO:HA	36:CE:98:GLY:HA2	1.71	0.44
50:AP:82:HIS:HA	50:AP:100:TYR:HB2	1.99	0.44
52:AA:49:LEU:HD11	52:AA:150:THR:HB	2.00	0.44
52:AA:149:ASN:ND2	52:AA:164:ASN:O	2.43	0.44
54:AY:9:ARG:HD3	54:AY:9:ARG:HA	1.71	0.44
63:AC:77:ILE:O	63:AC:81:LEU:N	2.45	0.44
64:AG:213:LEU:HD13	64:AG:216:GLN:HG2	2.00	0.44
66:AI:49:ARG:N	70:B2:338:C:OP1	2.49	0.44
69:A5:1292:G:H2'	69:A5:1294:U:P	2.57	0.44
69:A5:1343:A:N3	69:A5:3358:U:O2'	2.48	0.44
69:A5:2625:G:H21	69:A5:2649:A:H8	1.64	0.44
69:A5:3227:A:O2'	69:A5:3229:A:N6	2.47	0.44
70:B2:1390:U:H3	70:B2:1408:A:H1'	1.82	0.44
70:B2:1734:G:O6	81:AS:38:ARG:NH2	2.50	0.44
75:Ac:28:VAL:O	75:Ac:37:GLN:HB2	2.17	0.44
80:Cd:33:ILE:HG12	80:Cd:41:ARG:HD2	1.99	0.44
81:AS:24:ARG:HB2	81:AS:29:ALA:HB2	1.99	0.44
81:AS:124:ARG:HD2	81:AS:129:LEU:HD22	1.99	0.44
2:CL:76:THR:HG21	2:CL:103:ASN:HB2	1.99	0.44
10:CR:44:LEU:HD22	10:CR:49:LEU:HD12	1.98	0.44
13:CT:34:PHE:HB3	13:CT:64:ILE:HD13	1.98	0.44
15:CX:192:MET:HE2	15:CX:192:MET:HB2	1.91	0.44
21:CB:189:SER:OG	21:CB:192:ASP:OD2	2.36	0.44
23:Cc:65:MET:O	23:Cc:68:LYS:NZ	2.50	0.44
24:Ce:2:THR:OG1	24:Ce:3:ILE:N	2.50	0.44
26:Ci:19:LYS:HE3	26:Ci:19:LYS:HB3	1.88	0.44
26:Ci:40:LYS:HE3	69:A5:284:A:H2'	2.00	0.44
29:CC:236:ASP:N	29:CC:236:ASP:OD1	2.48	0.44
49:AR:44:LYS:HB3	49:AR:47:ARG:HD2	1.99	0.44
69:A5:395:A:O2'	69:A5:409:A:N1	2.48	0.44
69:A5:1783:A:N6	69:A5:1797:A:H2'	2.32	0.44
69:A5:3713:C:H42	69:A5:3769:C:N4	2.14	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:CU:262:LEU:HD13	76:CU:271:ILE:HG13	1.99	0.44
4:CM:144:LYS:HG3	69:A5:3791:A:H62	1.83	0.44
9:CQ:162:HIS:HA	69:A5:980:A:H5'	1.98	0.44
11:CA:105:SER:HB3	11:CA:160:SER:HB3	2.00	0.44
11:CA:113:ILE:HG13	11:CA:134:ALA:HB3	1.99	0.44
21:CB:85:ILE:HB	21:CB:165:HIS:CE1	2.53	0.44
30:Cm:120:ASN:OD1	30:Cm:120:ASN:N	2.42	0.44
37:CG:213:ASP:N	37:CG:213:ASP:OD1	2.50	0.44
44:AX:128:VAL:HG21	44:AX:140:ARG:HA	2.00	0.44
56:Aa:6:ARG:NH2	70:B2:1178:A:OP1	2.51	0.44
56:Aa:85:ARG:NH1	70:B2:1241:G:O5'	2.50	0.44
64:AG:226:GLU:H	64:AG:226:GLU:HG3	1.60	0.44
65:AH:30:GLU:HB3	65:AH:39:LEU:HB2	1.99	0.44
69:A5:1172:G:H4'	69:A5:1613:A:H4'	1.99	0.44
69:A5:1751:U:OP1	69:A5:2732:C:O2'	2.31	0.44
69:A5:2669:A:O2'	70:B2:1847:A:N1	2.46	0.44
70:B2:1169:C:N3	71:AW:20:ARG:NH1	2.65	0.44
81:AS:65:ASP:OD1	81:AS:65:ASP:N	2.48	0.44
1:CO:12:ASP:OD2	1:CO:39:ARG:NH1	2.51	0.44
1:CO:133:SER:O	1:CO:133:SER:OG	2.29	0.44
2:CL:16:TRP:HB3	2:CL:19:ARG:HH22	1.83	0.44
6:CN:159:ARG:HE	6:CN:165:THR:HG22	1.82	0.44
17:CZ:12:ILE:N	17:CZ:81:MET:O	2.45	0.44
18:Cr:16:ASN:HB2	29:CC:142:SER:HB2	2.00	0.44
22:CF:162:PHE:HA	22:CF:171:PRO:O	2.17	0.44
25:Cf:125:HIS:ND1	25:Cf:132:ARG:HD2	2.33	0.44
28:Cl:38:ASN:HB3	28:Cl:41:ARG:HG2	1.99	0.44
34:CJ:44:VAL:HG12	34:CJ:128:ILE:HD12	1.99	0.44
41:Ag:3:GLU:HA	41:Ag:316:SER:HA	2.00	0.44
49:AR:44:LYS:O	49:AR:47:ARG:N	2.51	0.44
50:AP:58:ALA:HA	50:AP:61:LYS:HB2	1.99	0.44
63:AC:170:LYS:HB3	63:AC:170:LYS:HE3	1.76	0.44
67:AQ:144:GLN:CD	67:AQ:145:LYS:H	2.26	0.44
69:A5:483:U:H3	69:A5:517:A:H61	1.65	0.44
70:B2:1079:A:OP1	70:B2:1980:U:O2'	2.34	0.44
70:B2:1358:G:N1	70:B2:1630:G:O6	2.50	0.44
72:AT:85:ASN:HB2	72:AT:91:HIS:HB3	1.99	0.44
74:AF:93:PRO:HB2	74:AF:95:VAL:HG22	2.00	0.44
75:Ac:38:ILE:HG13	75:Ac:39:ILE:H	1.83	0.44
4:CM:119:ARG:NH1	4:CM:120:ASN:OD1	2.51	0.44
13:CT:81:ARG:HA	13:CT:82:GLY:HA2	1.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:CY:124:LYS:HA	16:CY:124:LYS:HD2	1.85	0.44
21:CB:11:HIS:HB3	21:CB:235:TRP:O	2.18	0.44
29:CC:90:SER:HA	29:CC:91:GLY:HA2	1.63	0.44
29:CC:105:PHE:CZ	69:A5:811:G:H5'	2.52	0.44
42:AU:66:THR:HG22	42:AU:81:ARG:HG2	2.00	0.44
43:AO:50:ARG:NH1	51:AB:64:GLY:O	2.49	0.44
44:AX:71:ARG:HA	44:AX:82:THR:HA	1.98	0.44
44:AX:72:VAL:N	44:AX:81:ILE:O	2.45	0.44
50:AP:63:LEU:HD21	50:AP:93:THR:HG23	1.98	0.44
57:Ab:20:LYS:NZ	70:B2:1045:U:OP2	2.43	0.44
68:Cz:67:ILE:HD13	68:Cz:147:LYS:HE2	2.00	0.44
69:A5:663:U:C5	69:A5:751:A:H2'	2.53	0.44
69:A5:756:C:H1'	69:A5:3842:A:C5	2.53	0.44
69:A5:1619:C:H2'	69:A5:1620:A:C8	2.52	0.44
69:A5:2065:A:H5''	69:A5:2066:G:N7	2.33	0.44
70:B2:477:A:O2'	70:B2:851:A:N3	2.41	0.44
70:B2:837:A:H2'	70:B2:838:A:C8	2.53	0.44
70:B2:1079:A:C8	70:B2:1972:G:H1'	2.53	0.44
70:B2:1121:C:H42	70:B2:1189:G:H1	1.64	0.44
76:CU:272:ARG:HG2	76:CU:288:ILE:HG13	2.00	0.44
6:CN:52:GLY:HA3	6:CN:116:LEU:HD21	2.00	0.44
6:CN:57:GLN:HA	6:CN:58:GLY:HA2	1.71	0.44
6:CN:65:ARG:HB3	6:CN:129:TYR:HB3	2.00	0.44
10:CR:24:LEU:HD12	69:A5:1715:G:H4'	2.00	0.44
21:CB:196:TRP:O	21:CB:200:HIS:ND1	2.49	0.44
22:CF:105:ALA:HB3	22:CF:108:VAL:HG12	2.00	0.44
25:Cf:48:GLY:C	36:CE:232:LEU:HD23	2.43	0.44
30:Cm:98:LYS:HD2	30:Cm:118:THR:HG21	1.99	0.44
33:Co:26:TYR:OH	69:A5:3299:U:O2'	2.31	0.44
34:CJ:98:GLU:HG3	34:CJ:178:ILE:H	1.83	0.44
52:AA:12:GLU:HA	52:AA:15:ILE:HG12	1.99	0.44
55:AZ:102:HIS:HB3	55:AZ:105:GLN:HB3	2.00	0.44
62:AE:35:PRO:HB3	62:AE:145:ARG:NH2	2.32	0.44
64:AG:6:SER:HB3	64:AG:112:VAL:HG12	2.00	0.44
69:A5:83:U:H2'	69:A5:84:U:H6	1.83	0.44
69:A5:524:A:O2'	69:A5:526:U:OP1	2.28	0.44
70:B2:1758:A:C1'	81:AS:85:ASN:OD1	2.66	0.44
72:AT:122:LYS:HD3	72:AT:122:LYS:HA	1.74	0.44
8:CD:139:PRO:HB2	69:A5:1293:A:H1'	2.00	0.44
16:CY:17:ARG:O	16:CY:18:HIS:CD2	2.70	0.44
23:Cc:31:TYR:CZ	23:Cc:35:LEU:HD11	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Cf:60:LYS:HE3	25:Cf:60:LYS:HB3	1.89	0.44
35:CH:126:MET:HB3	35:CH:130:VAL:HG13	2.00	0.44
41:Ag:46:THR:HG1	41:Ag:48:ASP:CG	2.22	0.44
45:AM:40:HIS:O	70:B2:1314:G:O2'	2.32	0.44
49:AR:15:VAL:HG21	58:AD:212:VAL:HG21	1.98	0.44
50:AP:21:ARG:CA	81:AS:92:ASP:N	2.77	0.44
50:AP:21:ARG:HH12	50:AP:39:LEU:HA	1.83	0.44
52:AA:174:MET:HE3	52:AA:174:MET:HB3	1.79	0.44
55:AZ:44:ASN:OD1	55:AZ:44:ASN:N	2.51	0.44
57:Ab:3:LEU:HD23	57:Ab:3:LEU:HA	1.75	0.44
62:AE:193:GLY:HA2	62:AE:194:THR:HA	1.88	0.44
69:A5:669:U:OP2	69:A5:1592:U:O2'	2.21	0.44
69:A5:1712:C:H5	69:A5:1713:U:H6	1.65	0.44
69:A5:2735:A:H2'	69:A5:2736:A:C8	2.52	0.44
1:CO:87:ARG:HE	1:CO:87:ARG:HB3	1.60	0.43
15:CX:191:ARG:O	15:CX:196:ASN:OD1	2.36	0.43
18:Cr:95:LYS:HB2	18:Cr:95:LYS:HE3	1.76	0.43
26:Ci:41:ASN:HB3	69:A5:317:G:C8	2.52	0.43
32:Cp:81:SER:OG	32:Cp:82:ALA:N	2.51	0.43
40:A8:7:A:H2'	40:A8:8:A:C8	2.53	0.43
44:AX:90:SER:O	44:AX:90:SER:OG	2.36	0.43
51:AB:70:SER:OG	51:AB:71:LEU:N	2.50	0.43
61:AJ:166:PHE:HA	61:AJ:167:GLY:HA2	1.77	0.43
64:AG:106:MET:HE3	64:AG:106:MET:HB3	1.86	0.43
69:A5:868:A:O2'	69:A5:871:A:OP2	2.35	0.43
69:A5:2835:G:H2'	69:A5:2836:A:H3'	1.99	0.43
74:AF:134:PRO:HA	74:AF:137:VAL:HB	2.00	0.43
76:CU:277:GLU:HG2	76:CU:280:SER:HB3	2.00	0.43
7:CI:185:ARG:HB3	7:CI:190:LEU:HD12	1.99	0.43
16:CY:100:HIS:CG	69:A5:239:U:H4'	2.53	0.43
18:Cr:108:LYS:HB2	69:A5:1568:A:H62	1.83	0.43
21:CB:140:ASP:N	21:CB:140:ASP:OD1	2.51	0.43
23:Cc:34:THR:O	23:Cc:37:THR:OG1	2.27	0.43
26:Ci:47:THR:HA	26:Ci:50:MET:HG2	1.98	0.43
55:AZ:51:LYS:CD	81:AS:6:PRO:HG3	2.39	0.43
63:AC:87:ASP:HB3	63:AC:113:ILE:HG13	2.00	0.43
69:A5:433:U:H2'	69:A5:434:A:C8	2.53	0.43
69:A5:1583:G:H2'	69:A5:1584:A:C8	2.53	0.43
69:A5:2487:C:H1'	69:A5:3918:A:C8	2.53	0.43
70:B2:1681:U:OP2	70:B2:1707:A:N6	2.40	0.43
70:B2:1754:C:H2'	70:B2:1755:A:C8	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:AK:22:VAL:HG13	73:AK:64:HIS:HB3	2.00	0.43
8:CD:104:LEU:HD11	8:CD:108:ARG:HH21	1.83	0.43
8:CD:269:ASN:HA	39:A7:1:G:H4'	2.00	0.43
10:CR:18:GLY:HA3	69:A5:2190:A:H5''	2.00	0.43
15:CX:244:LYS:HA	15:CX:244:LYS:HD3	1.75	0.43
21:CB:141:LEU:H	21:CB:144:LYS:HB2	1.84	0.43
21:CB:395:ASP:OD1	21:CB:395:ASP:N	2.51	0.43
35:CH:27:ILE:HG21	35:CH:78:MET:HB3	1.98	0.43
36:CE:56:GLU:HG3	69:A5:1574:A:H4'	2.00	0.43
42:AU:55:PRO:HA	42:AU:91:ILE:HG13	1.99	0.43
47:AN:5:HIS:HE1	47:AN:121:ARG:HB3	1.81	0.43
50:AP:20:TYR:C	81:AS:91:ILE:HA	2.17	0.43
61:AJ:54:ILE:HB	61:AJ:78:LEU:HD11	2.00	0.43
64:AG:70:HIS:ND1	64:AG:103:ASP:OD2	2.51	0.43
64:AG:205:GLU:O	64:AG:209:ASP:N	2.51	0.43
66:AI:175:ALA:HA	66:AI:191:ILE:HA	2.01	0.43
68:Cz:103:LEU:H	69:A5:2873:C:H4'	1.83	0.43
68:Cz:105:LYS:HZ2	69:A5:2880:A:H5'	1.83	0.43
69:A5:801:G:O2'	69:A5:1676:A:OP1	2.32	0.43
69:A5:1580:U:O2'	69:A5:1581:G:O4'	2.32	0.43
69:A5:1711:C:H3'	69:A5:1712:C:C6	2.53	0.43
70:B2:222:C:O4'	70:B2:923:G:N2	2.51	0.43
70:B2:261:U:O4	70:B2:262:A:N6	2.51	0.43
70:B2:1737:U:H5'	81:AS:131:VAL:HG12	0.91	0.43
71:AW:30:CYS:HB2	71:AW:35:ILE:HD11	2.01	0.43
10:CR:96:MET:HG2	10:CR:100:ARG:HE	1.83	0.43
14:CP:8:SER:HB3	14:CP:149:ILE:HG21	2.00	0.43
15:CX:168:ARG:O	69:A5:1802:U:O2'	2.24	0.43
21:CB:122:TRP:O	21:CB:125:SER:OG	2.35	0.43
22:CF:99:ARG:HD2	22:CF:227:LYS:O	2.18	0.43
26:Ci:24:LYS:HB3	26:Ci:39:LEU:HD11	2.00	0.43
41:Ag:94:ALA:HA	41:Ag:95:ALA:HA	1.77	0.43
41:Ag:180:LEU:HD23	41:Ag:180:LEU:HA	1.84	0.43
41:Ag:263:ALA:HA	41:Ag:264:CYS:HA	1.83	0.43
53:AV:65:SER:HA	53:AV:68:SER:HB3	2.00	0.43
55:AZ:46:GLN:C	81:AS:23:LYS:CE	2.91	0.43
56:Aa:38:LYS:HE3	56:Aa:38:LYS:HB3	1.88	0.43
60:Af:130:VAL:HG21	60:Af:142:GLY:N	2.32	0.43
61:AJ:133:GLN:NE2	70:B2:520:A:O3'	2.50	0.43
65:AH:108:ASN:HB3	65:AH:110:LEU:HB2	2.00	0.43
67:AQ:6:ARG:HH21	67:AQ:101:TYR:HE2	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:Cz:40:ASN:OD1	68:Cz:200:ASN:ND2	2.48	0.43
69:A5:291:U:H2'	69:A5:292:G:C8	2.53	0.43
69:A5:850:A:H2'	69:A5:851:G:H8	1.82	0.43
69:A5:1963:U:H2'	69:A5:1964:A:H8	1.83	0.43
69:A5:2268:G:N2	69:A5:2473:C:O2	2.48	0.43
70:B2:604:C:H2'	70:B2:605:G:H8	1.83	0.43
70:B2:1182:C:O2	71:AW:16:ASN:ND2	2.42	0.43
70:B2:1821:G:N2	70:B2:1960:A:H8	2.16	0.43
80:Cd:108:VAL:HG11	80:Cd:114:LEU:HD22	1.99	0.43
1:CO:54:ILE:HG21	1:CO:54:ILE:HD13	1.81	0.43
6:CN:34:THR:O	6:CN:65:ARG:NH1	2.52	0.43
8:CD:112:LYS:HB2	8:CD:112:LYS:HE3	1.86	0.43
9:CQ:122:THR:OG1	9:CQ:124:ASP:OD1	2.33	0.43
16:CY:15:ARG:HH21	40:A8:21:U:H5''	1.83	0.43
17:CZ:4:ILE:HD12	17:CZ:4:ILE:HA	1.92	0.43
22:CF:231:TYR:HA	22:CF:235:GLY:HA2	2.00	0.43
25:Cf:53:LYS:HD3	25:Cf:76:GLU:HG3	1.99	0.43
25:Cf:97:LYS:HD2	25:Cf:113:ARG:HH12	1.84	0.43
29:CC:224:PHE:HD2	29:CC:230:ILE:HG21	1.83	0.43
31:Cn:18:ARG:NH2	70:B2:1214:A:OP2	2.46	0.43
45:AM:38:LEU:HD23	45:AM:38:LEU:HA	1.87	0.43
48:AL:37:VAL:O	70:B2:251:G:O2'	2.32	0.43
52:AA:24:HIS:HB3	52:AA:51:LEU:HD23	1.99	0.43
58:AD:41:VAL:HG23	58:AD:50:ILE:HB	2.00	0.43
64:AG:195:LEU:O	64:AG:199:ARG:N	2.47	0.43
68:Cz:124:LEU:HD22	68:Cz:128:LEU:HB2	2.01	0.43
68:Cz:133:LYS:NZ	69:A5:2880:A:OP2	2.50	0.43
69:A5:1461:G:H4'	69:A5:1478:A:H5''	2.01	0.43
69:A5:1702:G:N2	69:A5:1715:G:H22	2.16	0.43
69:A5:2171:U:O2'	79:Cg:12:SER:O	2.21	0.43
69:A5:3307:A:H2'	69:A5:3308:A:H8	1.83	0.43
70:B2:355:G:H5''	70:B2:357:A:H5'	2.00	0.43
70:B2:1880:C:O2	70:B2:1909:U:N3	2.52	0.43
70:B2:1889:G:N1	70:B2:1897:U:O2	2.51	0.43
4:CM:110:PHE:HB3	36:CE:220:LYS:HD2	2.01	0.43
13:CT:76:VAL:O	13:CT:87:LYS:N	2.39	0.43
14:CP:172:LYS:HA	14:CP:175:LEU:HB2	2.01	0.43
18:Cr:55:VAL:HG22	18:Cr:67:VAL:HG22	2.00	0.43
18:Cr:61:LYS:HA	18:Cr:62:LYS:HA	1.69	0.43
34:CJ:24:LYS:HG2	34:CJ:138:VAL:HG22	2.00	0.43
37:CG:99:LYS:HA	37:CG:102:LYS:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:AP:28:LEU:HG	50:AP:32:PRO:HG2	2.00	0.43
54:AY:112:ARG:HA	54:AY:115:MET:HE2	2.00	0.43
55:AZ:51:LYS:N	81:AS:6:PRO:HA	2.33	0.43
59:Ae:112:ARG:NH1	70:B2:512:U:OP1	2.51	0.43
63:AC:162:THR:HG22	63:AC:203:GLU:HB3	2.00	0.43
64:AG:191:ARG:HG2	64:AG:195:LEU:HD13	2.01	0.43
69:A5:3228:A:H2'	69:A5:3229:A:C8	2.54	0.43
70:B2:1651:C:OP2	81:AS:136:THR:CB	2.66	0.43
9:CQ:61:LEU:HD13	9:CQ:141:GLY:HA2	2.01	0.43
39:A7:67:G:N2	39:A7:108:G:H1	2.16	0.43
48:AL:31:LEU:H	48:AL:31:LEU:HG	1.58	0.43
52:AA:10:LEU:HD21	52:AA:15:ILE:HD13	2.00	0.43
67:AQ:82:GLN:HE22	70:B2:1674:C:H4'	1.83	0.43
68:Cz:38:LEU:HB2	68:Cz:163:LEU:HD12	1.99	0.43
69:A5:1144:C:H2'	69:A5:1145:C:C6	2.54	0.43
69:A5:1701:C:C5'	80:Cd:43:ILE:HG21	2.34	0.43
70:B2:106:C:O3'	70:B2:367:G:N2	2.47	0.43
70:B2:899:A:O2'	70:B2:901:G:OP2	2.36	0.43
70:B2:1274:U:H5	70:B2:1288:G:H22	1.67	0.43
70:B2:1319:A:H61	70:B2:1340:U:H3	1.65	0.43
1:CO:126:MET:HE2	1:CO:126:MET:HB3	1.86	0.43
4:CM:149:GLU:OE1	4:CM:158:GLY:N	2.51	0.43
9:CQ:32:TYR:HA	9:CQ:35:LEU:HB2	2.00	0.43
11:CA:117:GLU:OE2	11:CA:163:ARG:NH2	2.50	0.43
12:CS:95:ARG:NE	12:CS:113:MET:SD	2.84	0.43
15:CX:256:LYS:NZ	69:A5:1765:U:OP2	2.48	0.43
16:CY:35:SER:O	16:CY:39:ARG:N	2.42	0.43
18:Cr:105:LYS:HB3	18:Cr:105:LYS:HE2	1.59	0.43
21:CB:100:ARG:HD2	69:A5:3680:A:H4'	2.01	0.43
25:Cf:152:LEU:HD21	36:CE:238:PRO:HB3	1.99	0.43
29:CC:87:THR:O	29:CC:87:THR:OG1	2.36	0.43
40:A8:100:G:OP2	40:A8:102:A:O2'	2.35	0.43
45:AM:43:HIS:HB2	60:Af:130:VAL:HG12	2.00	0.43
50:AP:108:VAL:CG2	81:AS:118:ARG:HH21	2.24	0.43
51:AB:132:THR:OG1	51:AB:134:ASP:O	2.36	0.43
62:AE:104:ASP:N	62:AE:108:ARG:O	2.51	0.43
63:AC:189:SER:OG	63:AC:207:THR:OG1	2.24	0.43
69:A5:231:A:H4'	69:A5:233:A:N7	2.33	0.43
69:A5:620:U:N3	69:A5:622:A:N7	2.67	0.43
69:A5:908:C:C6	69:A5:910:C:H5'	2.53	0.43
69:A5:938:U:H2'	69:A5:963:G:H22	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:A5:3464:G:N2	69:A5:3467:A:O5'	2.39	0.43
70:B2:1067:G:H4'	70:B2:1971:A:H4'	2.00	0.43
1:CO:130:THR:OG1	1:CO:131:LEU:N	2.52	0.43
5:Ca:36:ALA:HA	5:Ca:37:GLY:HA2	1.75	0.43
11:CA:1:MET:HB2	11:CA:2:GLY:H	1.66	0.43
15:CX:229:HIS:O	15:CX:233:ALA:N	2.51	0.43
24:Ce:127:ARG:HH12	69:A5:1633:G:H5''	1.83	0.43
37:CG:195:LEU:HB3	37:CG:207:LEU:HD11	2.00	0.43
40:A8:40:A:OP2	77:Cj:65:GLN:NE2	2.36	0.43
41:Ag:5:LEU:HD13	41:Ag:271:LEU:HD21	2.00	0.43
41:Ag:157:PHE:HD1	41:Ag:166:ILE:HG22	1.84	0.43
48:AL:115:ARG:HD3	48:AL:115:ARG:HA	1.81	0.43
49:AR:44:LYS:O	49:AR:46:LEU:N	2.52	0.43
62:AE:38:LEU:O	62:AE:41:SER:OG	2.32	0.43
63:AC:159:LYS:HA	63:AC:160:PRO:HD2	1.85	0.43
69:A5:679:G:N2	69:A5:680:C:O4'	2.52	0.43
69:A5:751:A:N6	69:A5:1553:C:OP2	2.51	0.43
69:A5:1362:G:O2'	69:A5:1384:C:O2'	2.34	0.43
69:A5:1965:A:H2'	69:A5:1966:A:C8	2.47	0.43
70:B2:339:U:H2'	70:B2:340:A:H8	1.84	0.43
70:B2:1696:G:H4'	72:AT:41:LYS:HD3	2.01	0.43
4:CM:91:TRP:CD1	4:CM:94:LYS:HB2	2.54	0.43
11:CA:108:PRO:HG2	32:Cp:86:LEU:HB3	2.01	0.43
15:CX:250:ARG:HD2	15:CX:256:LYS:HE3	2.01	0.43
21:CB:341:LYS:HE2	21:CB:341:LYS:HB2	1.84	0.43
35:CH:157:ALA:O	35:CH:161:GLN:OE1	2.36	0.43
41:Ag:241:CYS:SG	41:Ag:242:PHE:N	2.92	0.43
43:AO:116:LEU:HD23	43:AO:116:LEU:HA	1.85	0.43
44:AX:130:LEU:HA	44:AX:133:LEU:HG	2.01	0.43
46:Ad:17:GLY:HA2	46:Ad:18:SER:HA	1.59	0.43
52:AA:184:ARG:HE	52:AA:189:ILE:HD11	1.84	0.43
56:Aa:44:ILE:HG13	56:Aa:45:VAL:HG13	2.00	0.43
58:AD:60:VAL:HG12	58:AD:68:ILE:HD13	2.01	0.43
62:AE:31:PRO:HB3	62:AE:43:PRO:HG3	1.99	0.43
62:AE:230:LYS:HB2	62:AE:233:LYS:HG3	2.00	0.43
69:A5:556:A:H2'	69:A5:557:G:H8	1.84	0.43
69:A5:1455:A:OP1	69:A5:1464:G:N2	2.52	0.43
69:A5:2578:U:H2'	69:A5:2579:G:H8	1.84	0.43
69:A5:2854:G:H2'	69:A5:2855:A:H8	1.84	0.43
69:A5:3360:G:H1	69:A5:3395:G:H1'	1.84	0.43
70:B2:1411:G:N2	70:B2:1412:A:O2'	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Ch:42:SER:OG	40:A8:76:A:O2'	2.26	0.42
25:Cf:47:HIS:CG	25:Cf:53:LYS:HB2	2.53	0.42
25:Cf:147:ARG:O	25:Cf:149:ARG:NH1	2.52	0.42
34:CJ:84:ALA:O	34:CJ:88:LEU:N	2.37	0.42
35:CH:51:ARG:HD2	69:A5:592:G:H5''	2.00	0.42
41:Ag:11:LEU:HD11	41:Ag:53:TYR:HB3	2.01	0.42
41:Ag:20:GLN:NE2	41:Ag:71:VAL:HG22	2.33	0.42
62:AE:45:LEU:HD23	62:AE:61:VAL:HG21	2.01	0.42
68:Cz:110:PHE:HB3	68:Cz:134:PHE:HD1	1.83	0.42
69:A5:935:A:H2	69:A5:968:U:H3	1.66	0.42
69:A5:1100:G:H1'	69:A5:1873:A:N6	2.34	0.42
69:A5:1418:A:H61	69:A5:1515:U:H2'	1.84	0.42
69:A5:3017:U:O2'	69:A5:3098:A:OP1	2.33	0.42
69:A5:3293:G:O2'	69:A5:3327:U:O4	2.34	0.42
70:B2:962:G:N2	70:B2:1024:C:O2'	2.44	0.42
70:B2:1079:A:H2	70:B2:1099:U:H3	1.67	0.42
73:AK:17:LYS:HD2	73:AK:89:PRO:HD2	2.00	0.42
6:CN:62:TYR:OH	38:A9:15:A:OP1	2.30	0.42
8:CD:48:LYS:HB3	8:CD:48:LYS:HE3	1.75	0.42
11:CA:51:ASP:HB3	11:CA:54:ARG:HB3	2.01	0.42
11:CA:149:LYS:HB3	11:CA:149:LYS:HE2	1.83	0.42
14:CP:3:ARG:NE	69:A5:416:C:H5''	2.34	0.42
18:Cr:21:LYS:HZ3	69:A5:1665:C:H5'	1.84	0.42
18:Cr:116:ARG:HD2	36:CE:75:VAL:HA	2.01	0.42
23:Cc:57:LYS:HE3	23:Cc:57:LYS:HB2	1.82	0.42
25:Cf:53:LYS:HB3	25:Cf:76:GLU:HB2	2.01	0.42
36:CE:44:LEU:HD12	36:CE:46:ARG:HH11	1.83	0.42
36:CE:171:LEU:HB3	36:CE:172:LYS:HB2	2.00	0.42
43:AO:66:ARG:NE	70:B2:992:A:OP1	2.51	0.42
45:AM:42:ILE:HG22	45:AM:115:VAL:HG21	2.01	0.42
55:AZ:72:VAL:HG12	55:AZ:78:ILE:HG23	2.00	0.42
67:AQ:1:MET:HG3	67:AQ:2:GLN:HE21	1.83	0.42
69:A5:806:A:H2'	69:A5:807:A:C8	2.54	0.42
69:A5:3611:C:OP1	80:Cd:75:ARG:HD3	2.19	0.42
69:A5:3716:C:H42	69:A5:3762:G:H1	1.65	0.42
69:A5:3960:U:H5'	80:Cd:20:ARG:HE	1.84	0.42
1:CO:124:ILE:HG21	12:CS:162:GLY:HA2	2.00	0.42
2:CL:3:LYS:O	2:CL:6:ASN:ND2	2.51	0.42
2:CL:64:ARG:NH1	2:CL:65:TYR:OH	2.52	0.42
2:CL:142:GLU:HB3	2:CL:144:LYS:H	1.84	0.42
3:CV:115:SER:O	3:CV:135:ASN:OD1	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Ca:91:LEU:HD21	5:Ca:98:LYS:HD3	2.00	0.42
15:CX:159:ARG:O	69:A5:4:U:O2'	2.33	0.42
17:CZ:55:LYS:N	69:A5:3007:G:OP1	2.51	0.42
26:CI:43:GLN:O	26:CI:47:THR:OG1	2.24	0.42
26:CI:85:ARG:HD2	26:CI:85:ARG:HA	1.81	0.42
35:CH:52:THR:OG1	35:CH:53:LEU:N	2.53	0.42
61:AJ:79:LEU:HD13	61:AJ:93:MET:HE3	2.01	0.42
64:AG:98:ARG:NH1	64:AG:101:ILE:O	2.44	0.42
65:AH:141:ARG:O	65:AH:153:LYS:N	2.50	0.42
69:A5:193:U:H2'	69:A5:194:A:C8	2.54	0.42
69:A5:677:G:N2	69:A5:746:G:N7	2.68	0.42
69:A5:1698:A:N6	80:CD:74:ILE:CG2	2.82	0.42
70:B2:613:A:OP2	70:B2:614:A:O2'	2.35	0.42
73:AK:3:MET:HB2	73:AK:7:HIS:CD2	2.54	0.42
80:CD:29:ARG:HH21	80:CD:49:PHE:HD1	1.67	0.42
1:CO:27:LYS:HD2	1:CO:27:LYS:HA	1.68	0.42
1:CO:190:ALA:HB3	1:CO:193:PRO:HD2	2.00	0.42
9:CQ:13:VAL:O	69:A5:1174:G:H5''	2.18	0.42
13:CT:135:PRO:HB2	22:CF:89:GLU:HB2	2.02	0.42
19:CH:62:HIS:ND1	40:A8:59:G:O6	2.36	0.42
22:CF:147:TYR:CE2	22:CF:241:GLU:HG3	2.54	0.42
29:CC:214:TYR:CE2	29:CC:217:ASP:HB2	2.55	0.42
29:CC:364:GLU:HB2	29:CC:366:ALA:N	2.35	0.42
39:A7:58:A:H2'	39:A7:59:G:C8	2.53	0.42
57:AB:51:GLN:NE2	70:B2:956:C:O2	2.53	0.42
58:AD:33:GLU:OE1	58:AD:59:GLN:NE2	2.52	0.42
67:AQ:32:GLY:H	67:AQ:69:ASP:HB3	1.84	0.42
68:Cz:70:ASP:H	68:Cz:72:GLN:HG2	1.84	0.42
69:A5:1118:C:H5''	69:A5:2517:A:C2	2.55	0.42
69:A5:2037:C:O2'	69:A5:2038:A:O5'	2.36	0.42
70:B2:29:U:H2'	70:B2:30:G:C8	2.55	0.42
70:B2:1600:A:OP2	70:B2:1601:A:N6	2.52	0.42
70:B2:1695:A:H1'	81:AS:83:PHE:CE2	2.49	0.42
73:AK:23:ALA:N	73:AK:64:HIS:O	2.52	0.42
74:AF:181:CYS:O	74:AF:185:ARG:NE	2.47	0.42
80:CD:41:ARG:O	80:CD:45:GLU:HG2	2.19	0.42
4:CM:1:MET:HE1	69:A5:621:A:H1'	2.02	0.42
9:CQ:16:THR:O	9:CQ:33:ARG:NH2	2.52	0.42
12:CS:85:ASP:HB2	12:CS:123:SER:HB3	2.02	0.42
15:CX:220:LEU:HD23	15:CX:220:LEU:HA	1.82	0.42
55:AZ:47:VAL:HG12	55:AZ:82:LEU:HD12	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:Ab:36:LYS:O	57:Ab:78:SER:OG	2.29	0.42
62:AE:201:HIS:N	62:AE:206:ASP:OD1	2.50	0.42
63:AC:54:ARG:HH22	63:AC:75:GLU:HB2	1.84	0.42
69:A5:40:U:O2'	69:A5:1008:A:N1	2.52	0.42
69:A5:286:A:N1	69:A5:313:A:H5'	2.35	0.42
69:A5:478:A:N1	69:A5:522:G:N2	2.67	0.42
69:A5:880:A:N6	69:A5:910:C:H5	2.18	0.42
69:A5:3429:A:H2'	69:A5:3431:C:H5''	2.02	0.42
69:A5:3898:C:H4'	80:Cd:23:THR:O	2.20	0.42
70:B2:270:G:O6	70:B2:293:A:N6	2.52	0.42
70:B2:1535:U:H2'	70:B2:1536:A:H8	1.83	0.42
74:AF:116:CYS:HA	74:AF:119:VAL:HG12	2.02	0.42
6:CN:96:ARG:HH22	6:CN:104:GLU:HG3	1.84	0.42
10:CR:94:LEU:HD12	10:CR:94:LEU:HA	1.79	0.42
16:CY:11:ARG:NH2	40:A8:21:U:OP1	2.53	0.42
17:CZ:59:LYS:HE3	17:CZ:59:LYS:HB3	1.87	0.42
21:CB:366:LYS:HE2	21:CB:366:LYS:HB3	1.78	0.42
27:Ck:33:LYS:NZ	69:A5:2063:A:OP2	2.38	0.42
34:CJ:103:ASN:N	69:A5:3205:G:OP1	2.45	0.42
36:CE:41:ARG:HD3	36:CE:41:ARG:H	1.84	0.42
36:CE:149:SER:O	36:CE:149:SER:OG	2.33	0.42
52:AA:79:SER:O	52:AA:84:GLN:NE2	2.52	0.42
56:Aa:60:ASP:N	56:Aa:60:ASP:OD1	2.51	0.42
59:Ae:103:ARG:NH1	70:B2:481:U:OP2	2.48	0.42
64:AG:148:SER:OG	64:AG:149:LYS:N	2.39	0.42
69:A5:522:G:O2'	69:A5:524:A:OP2	2.37	0.42
69:A5:1540:U:O4	69:A5:1541:A:N6	2.53	0.42
70:B2:1012:G:N2	70:B2:1075:U:O2	2.45	0.42
70:B2:1302:U:O4	70:B2:1642:C:O2'	2.36	0.42
70:B2:1361:C:O2	70:B2:1619:A:O2'	2.32	0.42
80:Cd:35:PHE:C	80:Cd:37:LYS:H	2.27	0.42
81:AS:36:VAL:HG13	81:AS:40:TYR:HD2	1.84	0.42
1:CO:111:PRO:HB3	69:A5:3802:U:C2	2.55	0.42
5:Ca:78:LYS:O	5:Ca:80:TRP:N	2.49	0.42
7:CI:116:ARG:HA	7:CI:117:GLY:HA2	1.81	0.42
8:CD:50:ARG:NH2	8:CD:72:ASP:OD2	2.40	0.42
14:CP:93:GLN:HE22	69:A5:402:A:H62	1.67	0.42
14:CP:177:ARG:HB3	69:A5:3777:U:OP2	2.19	0.42
18:Cr:80:ASN:OD1	18:Cr:83:ARG:N	2.43	0.42
25:Cf:47:HIS:HB2	25:Cf:76:GLU:OE1	2.20	0.42
29:CC:216:LYS:HE3	29:CC:216:LYS:HB3	1.75	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:CE:125:LEU:HD21	36:CE:163:LEU:HD23	2.02	0.42
41:Ag:24:ASN:HD21	41:Ag:76:GLY:HA2	1.85	0.42
45:AM:78:GLU:HB3	45:AM:79:HIS:H	1.67	0.42
51:AB:183:ASP:O	51:AB:185:LYS:N	2.53	0.42
51:AB:188:VAL:HG13	51:AB:191:LEU:HD11	2.02	0.42
52:AA:177:LEU:HA	52:AA:180:ARG:HB2	2.02	0.42
59:Ae:101:THR:O	59:Ae:105:LYS:N	2.53	0.42
65:AH:96:ARG:HD2	65:AH:123:VAL:HG23	2.00	0.42
67:AQ:91:SER:HA	67:AQ:94:LEU:HD22	2.02	0.42
1:CO:4:LEU:HD23	25:Cf:53:LYS:NZ	2.34	0.42
2:CL:46:PHE:CE2	19:Ch:118:LYS:HB2	2.55	0.42
4:CM:58:THR:HG22	69:A5:3754:C:N3	2.34	0.42
4:CM:158:GLY:HA2	4:CM:159:GLY:HA3	1.74	0.42
8:CD:211:LEU:HD21	8:CD:218:SER:HB2	2.01	0.42
11:CA:217:GLN:HE21	11:CA:217:GLN:HB2	1.54	0.42
12:CS:157:ARG:NH1	69:A5:3754:C:O5'	2.53	0.42
17:CZ:47:ASP:N	17:CZ:69:LYS:O	2.51	0.42
18:Cr:30:SER:OG	18:Cr:40:SER:N	2.53	0.42
21:CB:144:LYS:HD2	21:CB:144:LYS:HA	1.87	0.42
24:Ce:103:SER:HA	24:Ce:127:ARG:HH11	1.85	0.42
33:Co:12:CYS:HB3	33:Co:21:HIS:NE2	2.35	0.42
36:CE:237:TYR:HB3	36:CE:239:HIS:H	1.85	0.42
41:Ag:125:SER:OG	41:Ag:127:ASP:OD1	2.35	0.42
41:Ag:179:ASN:HD22	41:Ag:179:ASN:C	2.27	0.42
45:AM:43:HIS:NE2	70:B2:1341:C:OP2	2.49	0.42
62:AE:51:ARG:HB3	62:AE:111:ILE:HD11	2.01	0.42
68:Cz:63:MET:HE2	68:Cz:63:MET:HB2	1.63	0.42
70:B2:50:C:H2'	70:B2:429:C:H41	1.84	0.42
70:B2:890:U:O2	71:AW:124:LYS:NZ	2.34	0.42
70:B2:1651:C:C6	81:AS:136:THR:O	2.73	0.42
80:Cd:72:LYS:HB2	80:Cd:76:SER:O	2.20	0.42
81:AS:98:LEU:HD12	81:AS:102:ASN:HB2	2.00	0.42
5:Ca:47:ASP:OD2	9:CQ:178:ARG:NH2	2.53	0.42
5:Ca:47:ASP:OD1	5:Ca:47:ASP:N	2.53	0.42
8:CD:108:ARG:HA	8:CD:251:PRO:HB2	2.02	0.42
9:CQ:142:ARG:H	9:CQ:142:ARG:HG2	1.52	0.42
12:CS:137:THR:HG21	12:CS:146:HIS:CE1	2.55	0.42
14:CP:120:ASN:O	14:CP:145:HIS:N	2.51	0.42
14:CP:182:MET:HA	69:A5:3777:U:H1'	2.02	0.42
17:CZ:133:LEU:HB3	17:CZ:135:PHE:CZ	2.54	0.42
18:Cr:41:SER:OG	69:A5:1595:G:OP2	2.31	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Cr:47:ILE:HD11	18:Cr:79:LYS:HD2	2.02	0.42
18:Cr:57:PRO:HA	18:Cr:58:ALA:HA	1.76	0.42
18:Cr:80:ASN:HD21	18:Cr:85:ASP:HB2	1.84	0.42
20:Cb:47:ARG:NH2	69:A5:916:C:O2'	2.53	0.42
22:CF:172:ILE:HA	22:CF:177:VAL:HG21	2.02	0.42
22:CF:216:LYS:HB3	22:CF:216:LYS:HE2	1.76	0.42
32:Cp:22:LEU:HD21	69:A5:2529:G:H4'	2.02	0.42
33:Co:28:LYS:HD3	33:Co:28:LYS:HA	1.80	0.42
33:Co:35:ALA:HB3	33:Co:38:ARG:HB3	2.02	0.42
36:CE:46:ARG:NH2	69:A5:680:C:O2	2.50	0.42
41:Ag:11:LEU:HD21	41:Ag:53:TYR:HB3	2.01	0.42
41:Ag:63:HIS:HE1	41:Ag:81:SER:HB2	1.84	0.42
43:AO:120:ALA:HB2	43:AO:126:ILE:HD12	2.01	0.42
47:AN:10:GLY:HA2	70:B2:1160:A:H4'	2.02	0.42
51:AB:197:ALA:HA	51:AB:200:ILE:HG22	2.01	0.42
58:AD:56:LYS:HG3	58:AD:59:GLN:HB2	2.02	0.42
63:AC:188:VAL:HG11	70:B2:2:U:H3'	2.01	0.42
65:AH:143:ARG:NE	71:AW:51:GLU:OE1	2.53	0.42
69:A5:1170:U:N3	69:A5:1325:C:H5	2.17	0.42
69:A5:3307:A:H2'	69:A5:3308:A:C8	2.54	0.42
70:B2:1695:A:N1	81:AS:82:TRP:CD2	2.88	0.42
77:Cj:16:HIS:CD2	77:Cj:26:SER:O	2.73	0.42
8:CD:54:ARG:NH1	8:CD:147:ASP:O	2.43	0.42
11:CA:172:GLY:HA2	11:CA:173:GLY:HA2	1.66	0.42
13:CT:38:ASP:HB3	13:CT:64:ILE:HD12	2.01	0.42
14:CP:39:MET:HG2	14:CP:43:ARG:HG2	2.02	0.42
15:CX:204:THR:H	15:CX:207:ALA:HB3	1.84	0.42
18:Cr:9:TRP:O	18:Cr:13:ARG:N	2.52	0.42
22:CF:149:ASN:O	22:CF:153:VAL:HG23	2.20	0.42
25:Cf:6:ALA:HA	69:A5:559:A:H3'	2.02	0.42
25:Cf:54:ALA:HB3	25:Cf:148:ILE:HB	2.02	0.42
29:CC:191:ARG:NH1	69:A5:1629:C:H41	2.18	0.42
29:CC:212:VAL:HB	29:CC:232:THR:HG22	2.02	0.42
37:CG:107:TYR:HB2	37:CG:141:VAL:HG13	2.01	0.42
37:CG:141:VAL:HG12	37:CG:209:LEU:HD13	2.02	0.42
40:A8:46:C:O2'	40:A8:61:C:OP2	2.35	0.42
43:AO:74:ALA:HB1	43:AO:115:ALA:HB2	2.02	0.42
43:AO:140:THR:OG1	70:B2:1076:U:O2'	2.36	0.42
62:AE:208:VAL:HG13	62:AE:210:ILE:HD11	2.02	0.42
66:AI:119:LEU:HD21	66:AI:155:GLN:HE21	1.83	0.42
69:A5:30:A:H4'	69:A5:347:A:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:A5:762:G:H5'	69:A5:767:A:N6	2.35	0.42
69:A5:942:A:H2'	69:A5:959:U:H3	1.85	0.42
69:A5:1232:G:N1	69:A5:1247:U:O2	2.53	0.42
69:A5:2657:A:H2	69:A5:2664:U:N3	2.18	0.42
69:A5:3133:A:H2'	69:A5:3134:G:C8	2.54	0.42
69:A5:3280:A:C5	69:A5:3281:G:H1'	2.55	0.42
70:B2:1284:A:OP2	70:B2:1656:G:N2	2.43	0.42
80:Cd:35:PHE:HA	80:Cd:38:ARG:HG2	2.02	0.42
3:CV:109:LYS:HE2	3:CV:109:LYS:HB2	1.92	0.41
4:CM:47:ARG:NH2	4:CM:68:ALA:O	2.50	0.41
4:CM:147:ARG:HE	69:A5:3790:A:H61	1.67	0.41
10:CR:140:GLU:HG3	69:A5:2471:A:H62	1.85	0.41
11:CA:69:TYR:HB3	69:A5:3003:C:N1	2.35	0.41
17:CZ:98:LYS:HD3	17:CZ:98:LYS:HA	1.79	0.41
36:CE:170:ARG:NH2	69:A5:759:U:OP2	2.52	0.41
54:AY:90:TYR:OH	70:B2:449:C:OP1	2.31	0.41
66:AI:2:GLY:N	70:B2:398:C:OP2	2.53	0.41
68:Cz:51:GLY:HA3	68:Cz:193:LEU:HD11	2.02	0.41
69:A5:474:A:N6	69:A5:523:C:O2'	2.43	0.41
69:A5:1196:A:H2'	69:A5:1197:A:C8	2.55	0.41
69:A5:1594:U:C6	69:A5:1599:C:H1'	2.56	0.41
69:A5:1738:U:H5	69:A5:2151:A:N1	2.18	0.41
69:A5:2564:U:H2'	69:A5:2565:G:O4'	2.20	0.41
69:A5:2837:A:H2'	69:A5:2838:U:H2'	2.02	0.41
70:B2:189:C:H1'	70:B2:190:U:H5	1.85	0.41
70:B2:492:G:N1	70:B2:507:C:O2	2.53	0.41
70:B2:913:G:O2'	70:B2:930:G:O6	2.37	0.41
1:CO:39:ARG:NH2	69:A5:3723:A:O5'	2.52	0.41
6:CN:141:ALA:HB2	69:A5:129:A:H4'	2.01	0.41
9:CQ:33:ARG:HH11	9:CQ:33:ARG:HD2	1.67	0.41
9:CQ:154:LYS:HA	9:CQ:154:LYS:HD2	1.92	0.41
23:Cc:48:ILE:HG21	23:Cc:60:ILE:HG21	2.01	0.41
24:Ce:127:ARG:NH1	69:A5:1633:G:H5''	2.35	0.41
36:CE:214:LYS:HA	36:CE:223:ALA:HB1	2.03	0.41
48:AL:35:ARG:HH12	48:AL:64:ARG:HE	1.67	0.41
51:AB:25:PHE:HA	51:AB:28:LYS:HD2	2.02	0.41
51:AB:184:LEU:HB3	51:AB:188:VAL:HG23	2.01	0.41
52:AA:181:GLU:OE1	52:AA:184:ARG:NH1	2.52	0.41
56:Aa:89:ARG:HA	56:Aa:92:ARG:HD2	2.02	0.41
59:Ae:77:SER:OG	59:Ae:78:LEU:N	2.52	0.41
63:AC:125:LYS:HB2	63:AC:140:LEU:HD12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:AI:146:LYS:HB3	66:AI:147:VAL:H	1.75	0.41
68:Cz:72:GLN:HG3	68:Cz:73:HIS:HD2	1.86	0.41
69:A5:214:A:H1'	69:A5:240:G:C8	2.54	0.41
69:A5:262:G:H21	69:A5:263:A:H62	1.67	0.41
69:A5:415:A:H5''	69:A5:415:A:H8	1.85	0.41
69:A5:1391:A:N3	69:A5:1543:C:O2'	2.50	0.41
69:A5:1793:C:H2'	69:A5:1795:A:O4'	2.20	0.41
69:A5:2229:A:N3	69:A5:2499:U:H2'	2.36	0.41
69:A5:2845:G:N7	69:A5:2846:A:N6	2.68	0.41
69:A5:3370:A:N6	69:A5:3382:G:O2'	2.53	0.41
69:A5:3711:G:H1	69:A5:3848:U:H2'	1.85	0.41
70:B2:219:A:H2'	70:B2:220:A:C8	2.55	0.41
70:B2:610:U:H2'	70:B2:611:U:C6	2.55	0.41
70:B2:819:G:H2'	70:B2:820:G:C8	2.55	0.41
1:CO:110:ILE:HD13	1:CO:110:ILE:HG21	1.75	0.41
3:CV:25:VAL:HG22	3:CV:38:TYR:HD2	1.84	0.41
8:CD:245:GLN:O	8:CD:249:ASN:ND2	2.36	0.41
12:CS:165:LYS:HD3	12:CS:165:LYS:HA	1.86	0.41
15:CX:173:LEU:HA	15:CX:173:LEU:HD12	1.82	0.41
21:CB:223:THR:HA	21:CB:338:ILE:HG22	2.01	0.41
21:CB:224:LYS:NZ	69:A5:3584:C:OP2	2.48	0.41
27:Ck:35:LYS:NZ	69:A5:2063:A:OP1	2.53	0.41
30:Cm:97:ARG:HD2	30:Cm:120:ASN:HB2	2.02	0.41
44:AX:107:ARG:HD3	44:AX:112:VAL:HA	2.01	0.41
50:AP:10:LYS:HD3	50:AP:10:LYS:HA	1.88	0.41
50:AP:62:LYS:HA	50:AP:65:LYS:HB2	2.02	0.41
51:AB:35:ALA:HB2	51:AB:44:ILE:HD11	2.01	0.41
51:AB:66:VAL:HG11	51:AB:88:ARG:HE	1.85	0.41
51:AB:119:LYS:O	51:AB:121:GLN:N	2.52	0.41
51:AB:212:ASP:OD1	51:AB:212:ASP:N	2.53	0.41
52:AA:113:GLN:HA	52:AA:114:PRO:HD3	1.93	0.41
53:AV:71:ARG:NE	57:Ab:3:LEU:HD12	2.36	0.41
55:AZ:46:GLN:NE2	81:AS:23:LYS:C	2.78	0.41
61:AJ:151:ARG:NH2	70:B2:847:G:O4'	2.53	0.41
69:A5:1418:A:N6	69:A5:1515:U:H2'	2.34	0.41
69:A5:2660:U:OP1	69:A5:3504:G:O2'	2.25	0.41
69:A5:3588:G:H2'	69:A5:3589:G:C8	2.53	0.41
70:B2:62:A:N3	70:B2:292:G:N2	2.68	0.41
70:B2:922:G:H2'	70:B2:923:G:C8	2.55	0.41
81:AS:24:ARG:HH21	81:AS:29:ALA:HA	1.85	0.41
2:CL:190:ARG:HH22	69:A5:3307:A:P	2.43	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CN:54:ARG:HD3	6:CN:54:ARG:HA	1.80	0.41
8:CD:183:TYR:CD2	8:CD:190:PHE:HA	2.55	0.41
8:CD:286:LYS:NZ	39:A7:63:C:N3	2.66	0.41
11:CA:49:ILE:HD11	11:CA:75:LEU:HD21	2.03	0.41
12:CS:17:LEU:HA	12:CS:18:PRO:HD3	1.91	0.41
15:CX:198:ILE:HD12	15:CX:237:LEU:HD12	2.01	0.41
21:CB:189:SER:OG	21:CB:189:SER:O	2.33	0.41
25:Cf:110:ARG:HH11	25:Cf:110:ARG:HD3	1.70	0.41
29:CC:70:TRP:CD1	29:CC:70:TRP:H	2.38	0.41
29:CC:350:THR:O	29:CC:354:VAL:HG22	2.20	0.41
43:AO:95:ILE:HG21	43:AO:116:LEU:HD21	2.02	0.41
53:AV:15:ARG:HG2	63:AC:242:MET:HE1	2.02	0.41
58:AD:29:ARG:HG3	73:AK:59:GLN:HB2	2.01	0.41
58:AD:124:VAL:HA	58:AD:127:TYR:HB3	2.02	0.41
61:AJ:126:HIS:HD2	61:AJ:130:LEU:HD23	1.86	0.41
65:AH:101:LYS:HD2	65:AH:101:LYS:HA	1.80	0.41
69:A5:1056:G:OP1	69:A5:2035:C:O2'	2.27	0.41
70:B2:1128:C:H2'	70:B2:1129:A:C8	2.55	0.41
70:B2:1727:U:H4'	70:B2:1728:G:N1	2.35	0.41
72:AT:97:ASP:N	72:AT:97:ASP:OD1	2.53	0.41
7:CI:101:LYS:HB2	7:CI:101:LYS:HE3	1.76	0.41
7:CI:116:ARG:HB3	69:A5:3150:G:H5''	2.02	0.41
8:CD:99:TYR:CE1	8:CD:164:LYS:HB3	2.52	0.41
21:CB:217:ILE:HD12	21:CB:333:ILE:HD11	2.01	0.41
22:CF:94:PHE:HB2	22:CF:148:PRO:HG3	2.03	0.41
34:CJ:18:ARG:HG3	34:CJ:160:HIS:CE1	2.56	0.41
36:CE:88:LYS:HB3	36:CE:89:ARG:H	1.77	0.41
41:Ag:5:LEU:HB2	41:Ag:271:LEU:HD11	2.02	0.41
41:Ag:233:HIS:HD2	41:Ag:251:VAL:HG21	1.85	0.41
43:AO:50:ARG:HD3	51:AB:65:ARG:HD3	2.00	0.41
45:AM:31:LYS:HD2	73:AK:82:HIS:CE1	2.56	0.41
56:Aa:92:ARG:HH22	70:B2:1821:G:P	2.43	0.41
62:AE:183:ILE:HD12	62:AE:220:THR:HG21	2.03	0.41
65:AH:127:ILE:O	65:AH:131:LEU:N	2.54	0.41
69:A5:291:U:H2'	69:A5:292:G:H8	1.85	0.41
69:A5:1528:G:H2'	69:A5:1529:C:H6	1.85	0.41
69:A5:2115:U:O2	79:Cg:62:ARG:NH2	2.53	0.41
80:Cd:24:ILE:HG23	80:Cd:81:ILE:HG23	2.03	0.41
81:AS:69:THR:OG1	81:AS:73:ASN:ND2	2.53	0.41
5:Ca:148:SER:OG	5:Ca:149:ALA:OXT	2.37	0.41
6:CN:53:TYR:CE1	6:CN:61:ILE:HD11	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CD:68:ARG:HD3	8:CD:68:ARG:HA	1.66	0.41
9:CQ:78:SER:O	9:CQ:99:THR:OG1	2.39	0.41
11:CA:156:LYS:HE3	11:CA:156:LYS:HB3	1.92	0.41
14:CP:179:LYS:HA	14:CP:179:LYS:HD3	1.85	0.41
22:CF:223:GLY:HA3	69:A5:1382:U:H4'	2.02	0.41
46:Ad:40:ARG:HA	46:Ad:43:PHE:HB3	2.02	0.41
49:AR:85:VAL:HG13	49:AR:88:VAL:HB	2.02	0.41
62:AE:11:ARG:NH1	62:AE:21:ASP:OD1	2.53	0.41
67:AQ:18:LYS:HD3	67:AQ:19:LYS:HG3	2.02	0.41
67:AQ:111:LYS:HD2	67:AQ:114:LEU:HB2	2.02	0.41
68:Cz:28:PHE:CD2	69:A5:2848:A:H4'	2.56	0.41
69:A5:631:A:C2	69:A5:633:A:H5'	2.56	0.41
69:A5:773:G:H21	69:A5:775:U:H5	1.69	0.41
69:A5:839:A:H5''	69:A5:840:U:C4	2.56	0.41
69:A5:871:A:H5'	69:A5:872:A:H2	1.86	0.41
69:A5:1100:G:H2'	69:A5:1101:A:C8	2.56	0.41
69:A5:3108:U:H2'	69:A5:3109:A:C8	2.56	0.41
69:A5:3788:G:H22	69:A5:3824:C:H42	1.68	0.41
70:B2:1174:A:H2'	70:B2:1175:A:C8	2.56	0.41
2:CL:166:PHE:CE2	5:Ca:83:VAL:HA	2.56	0.41
5:Ca:1:MET:HE3	5:Ca:1:MET:HB2	1.86	0.41
6:CN:14:LYS:HD2	69:A5:287:G:C4	2.56	0.41
7:CI:26:VAL:HA	7:CI:27:PRO:HD3	1.86	0.41
9:CQ:35:LEU:HA	9:CQ:35:LEU:HD23	1.81	0.41
12:CS:15:ARG:HH11	12:CS:15:ARG:HD2	1.70	0.41
13:CT:128:LEU:HD13	69:A5:1310:A:H2	1.86	0.41
18:Cr:39:VAL:HG23	18:Cr:41:SER:HB2	2.02	0.41
29:CC:233:ILE:HD11	29:CC:239:ASN:H	1.86	0.41
36:CE:19:LYS:HA	36:CE:19:LYS:HD2	1.81	0.41
42:AU:32:ARG:NH1	70:B2:1577:A:OP1	2.53	0.41
45:AM:68:TYR:CG	60:Af:104:LYS:HD3	2.56	0.41
50:AP:117:HIS:CE1	81:AS:117:ILE:CD1	3.04	0.41
52:AA:102:ARG:NH2	70:B2:1408:A:OP1	2.44	0.41
54:AY:92:LEU:HD22	54:AY:97:LEU:HD12	2.03	0.41
61:AJ:66:GLU:HA	61:AJ:67:LYS:HA	1.75	0.41
63:AC:234:LEU:HD23	71:AW:68:ARG:HA	2.01	0.41
65:AH:158:LYS:HD2	65:AH:161:GLN:HB2	2.03	0.41
67:AQ:15:PHE:O	67:AQ:92:LYS:NZ	2.47	0.41
67:AQ:76:GLY:O	67:AQ:82:GLN:NE2	2.53	0.41
68:Cz:110:PHE:H	68:Cz:135:PRO:HD2	1.86	0.41
69:A5:147:A:H3'	69:A5:148:U:H4'	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:A5:395:A:N6	69:A5:418:G:O2'	2.53	0.41
69:A5:931:A:C5	69:A5:932:G:H1'	2.55	0.41
69:A5:1215:A:N6	69:A5:1263:U:O2'	2.53	0.41
69:A5:1542:C:H2'	69:A5:1543:C:H6	1.85	0.41
70:B2:65:A:N6	70:B2:83:A:OP2	2.51	0.41
70:B2:264:C:N3	70:B2:265:A:N6	2.68	0.41
70:B2:1174:A:H5'	70:B2:1385:U:C5	2.55	0.41
70:B2:1182:C:H1'	71:AW:16:ASN:HD21	1.86	0.41
70:B2:1992:A:O2'	70:B2:1993:U:O4'	2.39	0.41
6:CN:47:LYS:HG2	6:CN:119:TYR:CD1	2.55	0.41
11:CA:177:LYS:HG2	32:Cp:26:VAL:HG23	2.03	0.41
16:CY:62:PHE:O	16:CY:64:GLY:N	2.46	0.41
17:CZ:68:VAL:N	17:CZ:118:GLU:OE2	2.54	0.41
18:Cr:44:TYR:OH	69:A5:1593:U:OP2	2.28	0.41
21:CB:226:LYS:HB2	21:CB:272:LYS:HG2	2.02	0.41
25:Cf:110:ARG:HE	25:Cf:113:ARG:N	2.16	0.41
44:AX:135:LYS:H	44:AX:135:LYS:HG2	1.69	0.41
47:AN:100:LYS:HA	47:AN:103:GLU:HG2	2.02	0.41
48:AL:53:ILE:HG13	48:AL:54:ASP:H	1.85	0.41
54:AY:53:PRO:HA	54:AY:56:VAL:HG23	2.03	0.41
58:AD:41:VAL:HB	58:AD:50:ILE:HD12	2.02	0.41
66:AI:56:ARG:NH2	70:B2:337:U:OP1	2.49	0.41
69:A5:3719:A:H1'	69:A5:3764:G:C8	2.56	0.41
70:B2:1174:A:H5'	70:B2:1385:U:H5	1.86	0.41
73:AK:78:ARG:HB3	73:AK:83:LEU:HD12	2.03	0.41
74:AF:139:VAL:HA	74:AF:142:ILE:HG12	2.03	0.41
74:AF:156:ARG:NH1	75:Ac:20:GLN:HB3	2.35	0.41
74:AF:161:ARG:HB2	74:AF:229:ASN:HB3	2.02	0.41
74:AF:171:ARG:CZ	75:Ac:45:PRO:HD3	2.51	0.41
80:Cd:38:ARG:HA	80:Cd:39:ALA:HA	1.74	0.41
2:CL:150:LYS:HB2	2:CL:150:LYS:HE3	1.76	0.41
5:Ca:100:PRO:HD2	5:Ca:123:VAL:HG12	2.03	0.41
13:CT:93:ILE:HD13	13:CT:93:ILE:HA	1.86	0.41
15:CX:190:ASN:N	15:CX:190:ASN:OD1	2.51	0.41
15:CX:216:THR:HA	15:CX:260:ARG:HA	2.03	0.41
17:CZ:4:ILE:HG12	23:Cc:66:LEU:HB3	2.02	0.41
17:CZ:50:PRO:HD3	17:CZ:68:VAL:HG22	2.03	0.41
18:Cr:51:LYS:HB3	69:A5:1593:U:O4	2.20	0.41
22:CF:127:LYS:HB2	22:CF:127:LYS:HE3	1.91	0.41
23:Cc:99:PRO:HB3	23:Cc:104:ILE:HD11	2.03	0.41
24:Ce:18:HIS:O	24:Ce:52:TYR:OH	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Cf:50:LEU:HB2	69:A5:3714:U:C5	2.55	0.41
25:Cf:68:GLU:H	25:Cf:68:GLU:HG2	1.37	0.41
28:Cl:41:ARG:HD2	28:Cl:41:ARG:HA	1.84	0.41
35:CH:15:ASP:OD1	35:CH:15:ASP:N	2.46	0.41
35:CH:43:LEU:HD23	35:CH:45:MET:HE2	2.03	0.41
37:CG:180:ARG:HD3	37:CG:232:ASN:HA	2.02	0.41
40:A8:18:C:H2'	40:A8:19:A:C8	2.56	0.41
41:Ag:11:LEU:HB2	41:Ag:308:ILE:HG23	2.01	0.41
41:Ag:132:LEU:HD21	41:Ag:141:PHE:HB3	2.03	0.41
41:Ag:133:TRP:CE2	41:Ag:139:CYS:HB2	2.56	0.41
41:Ag:184:LYS:HE3	41:Ag:184:LYS:HB3	1.93	0.41
43:AO:125:LYS:HD2	43:AO:125:LYS:HA	1.79	0.41
47:AN:70:LYS:NZ	70:B2:1050:A:OP2	2.43	0.41
51:AB:77:ASP:OD2	51:AB:82:ARG:NH2	2.50	0.41
54:AY:103:GLN:H	54:AY:104:THR:HA	1.86	0.41
55:AZ:49:PHE:CZ	81:AS:6:PRO:HD3	2.20	0.41
61:AJ:87:VAL:HB	61:AJ:109:ARG:HG3	2.02	0.41
61:AJ:137:ARG:HB2	61:AJ:161:SER:HB3	2.02	0.41
62:AE:9:LEU:HB3	62:AE:30:ARG:HD3	2.03	0.41
62:AE:29:PRO:HB2	62:AE:43:PRO:HG2	2.03	0.41
62:AE:63:LYS:O	62:AE:67:GLN:OE1	2.39	0.41
64:AG:7:TYR:HB3	64:AG:10:THR:HG22	2.03	0.41
64:AG:79:LYS:HA	64:AG:80:GLY:HA2	1.81	0.41
65:AH:169:ASP:O	65:AH:173:SER:OG	2.28	0.41
67:AQ:62:LYS:HA	67:AQ:65:PHE:HB2	2.03	0.41
67:AQ:132:LYS:HB3	70:B2:1797:G:H5'	2.02	0.41
69:A5:376:G:N2	69:A5:379:A:OP2	2.40	0.41
69:A5:449:U:H2'	69:A5:450:G:C8	2.56	0.41
69:A5:462:C:H1'	69:A5:537:A:H1'	2.03	0.41
69:A5:1137:G:N2	69:A5:1161:C:OP1	2.54	0.41
69:A5:1689:G:H1	69:A5:2734:A:N6	2.19	0.41
69:A5:2032:U:H4'	69:A5:2045:U:H4'	2.03	0.41
69:A5:2219:U:O2'	69:A5:2221:G:N7	2.47	0.41
69:A5:2477:C:H2'	69:A5:2478:A:C8	2.53	0.41
69:A5:3795:G:N2	69:A5:3814:U:H3	2.17	0.41
70:B2:204:C:N4	70:B2:267:G:O6	2.54	0.41
70:B2:1651:C:C6	81:AS:136:THR:OG1	2.74	0.41
70:B2:1696:G:O2'	70:B2:1755:A:O2'	2.28	0.41
70:B2:1736:U:H3'	81:AS:131:VAL:HG21	0.89	0.41
70:B2:1758:A:H1'	81:AS:85:ASN:OD1	2.20	0.41
70:B2:1783:U:H2'	70:B2:1784:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:AT:8:ASP:OD1	72:AT:8:ASP:N	2.45	0.41
72:AT:85:ASN:HB3	72:AT:86:GLY:H	1.63	0.41
10:CR:28:GLU:HG3	10:CR:49:LEU:HD22	2.01	0.41
13:CT:5:LYS:HA	13:CT:6:GLY:HA2	1.90	0.41
13:CT:82:GLY:HA3	20:Cb:16:ALA:HB1	2.01	0.41
13:CT:135:PRO:HD3	22:CF:128:LEU:O	2.21	0.41
23:Cc:57:LYS:HD3	23:Cc:73:HIS:HE1	1.86	0.41
26:Ci:60:HIS:HB2	26:Ci:65:LYS:HG3	2.03	0.41
29:CC:192:PHE:O	69:A5:1661:C:N4	2.46	0.41
37:CG:88:PHE:HB3	37:CG:188:ILE:HG21	2.02	0.41
50:AP:20:TYR:CG	81:AS:90:ILE:HG23	2.55	0.41
53:AV:11:LEU:HD23	53:AV:11:LEU:HA	1.93	0.41
55:AZ:53:THR:O	55:AZ:57:LEU:N	2.54	0.41
63:AC:54:ARG:HB3	63:AC:263:LEU:HG	2.02	0.41
67:AQ:33:LEU:HD13	67:AQ:35:LYS:HE3	2.03	0.41
70:B2:420:U:O2'	70:B2:423:G:O6	2.25	0.41
70:B2:649:U:H2'	70:B2:650:G:C8	2.56	0.41
70:B2:1258:G:H21	70:B2:1763:C:H4'	1.85	0.41
70:B2:1563:C:H2'	70:B2:1564:A:C8	2.56	0.41
71:AW:14:ILE:HG13	71:AW:27:LEU:HD21	2.02	0.41
71:AW:38:LEU:O	71:AW:42:MET:N	2.50	0.41
74:AF:212:ASN:HB2	74:AF:214:TYR:CE2	2.56	0.41
75:Ac:30:PHE:HZ	75:Ac:54:LEU:HD11	1.85	0.41
81:AS:60:THR:OG1	81:AS:61:GLU:N	2.52	0.41
9:CQ:45:ARG:HD3	69:A5:1182:A:C6	2.56	0.40
9:CQ:65:ARG:NE	69:A5:872:A:H2'	2.35	0.40
9:CQ:181:ARG:HE	9:CQ:181:ARG:HB2	1.55	0.40
11:CA:24:LYS:HA	11:CA:24:LYS:HD2	1.90	0.40
11:CA:98:ILE:H	11:CA:98:ILE:HG13	1.66	0.40
11:CA:233:ARG:O	11:CA:235:VAL:N	2.54	0.40
21:CB:116:ARG:HH22	69:A5:3889:U:P	2.44	0.40
29:CC:203:ARG:HG3	29:CC:204:ARG:H	1.86	0.40
36:CE:56:GLU:HB3	36:CE:58:ALA:HB2	2.01	0.40
42:AU:31:VAL:HA	42:AU:34:LEU:HD23	2.04	0.40
44:AX:73:GLN:HB2	44:AX:80:LYS:HG2	2.03	0.40
44:AX:94:ILE:HD13	44:AX:94:ILE:HA	1.89	0.40
45:AM:60:ALA:H	45:AM:69:LYS:HZ1	1.69	0.40
49:AR:94:ASP:H	49:AR:95:ILE:HA	1.86	0.40
52:AA:139:TYR:CZ	70:B2:1382:G:H4'	2.57	0.40
56:Aa:13:HIS:HE1	70:B2:1021:A:C8	2.39	0.40
60:Af:95:ARG:HH11	70:B2:1332:G:H21	1.68	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:AH:107:ARG:HD3	65:AH:107:ARG:HA	1.88	0.40
65:AH:116:ARG:O	65:AH:119:THR:OG1	2.32	0.40
67:AQ:96:ALA:O	67:AQ:100:LYS:NZ	2.53	0.40
68:Cz:160:LYS:HB3	68:Cz:164:CYS:H	1.85	0.40
69:A5:677:G:H1	69:A5:744:U:H3	1.69	0.40
69:A5:1654:C:H2'	69:A5:1655:A:H8	1.86	0.40
69:A5:3131:C:H2'	69:A5:3132:C:C6	2.57	0.40
69:A5:3626:A:H1'	69:A5:3627:C:H2'	2.03	0.40
69:A5:3710:U:H1'	69:A5:3711:G:H21	1.86	0.40
70:B2:369:G:O2'	70:B2:838:A:N6	2.54	0.40
74:AF:48:ARG:NH1	74:AF:124:GLU:HB3	2.34	0.40
74:AF:96:GLU:O	74:AF:99:THR:OG1	2.30	0.40
76:CU:200:ILE:HD12	76:CU:200:ILE:HA	1.92	0.40
5:Ca:147:LEU:HD12	5:Ca:147:LEU:HA	1.98	0.40
7:CI:46:PHE:HB3	7:CI:139:ARG:HG2	2.04	0.40
11:CA:130:SER:O	11:CA:130:SER:OG	2.36	0.40
23:Cc:35:LEU:HD22	23:Cc:63:TYR:CD2	2.56	0.40
24:Ce:7:TYR:HD2	36:CE:80:SER:H	1.68	0.40
25:Cf:50:LEU:HB3	25:Cf:151:MET:SD	2.61	0.40
34:CJ:118:ILE:HD13	34:CJ:124:TYR:HD1	1.87	0.40
35:CH:69:ARG:NH1	69:A5:3647:A:H5'	2.36	0.40
41:Ag:63:HIS:CE1	41:Ag:81:SER:HB2	2.56	0.40
48:AL:30:LEU:HD12	48:AL:30:LEU:HA	1.90	0.40
52:AA:7:ILE:HG22	53:AV:42:GLU:HB2	2.03	0.40
58:AD:10:LYS:NZ	70:B2:1680:G:OP2	2.44	0.40
62:AE:92:LEU:HB2	62:AE:97:GLU:HB2	2.02	0.40
62:AE:204:SER:OG	62:AE:205:PHE:N	2.51	0.40
64:AG:30:LYS:HE2	64:AG:36:VAL:HB	2.03	0.40
69:A5:522:G:O2'	69:A5:525:U:OP1	2.38	0.40
69:A5:829:U:H2'	69:A5:830:U:C6	2.57	0.40
69:A5:1315:A:H8	69:A5:1315:A:OP2	2.03	0.40
69:A5:1699:A:H2	80:Cd:70:TRP:CE2	2.39	0.40
69:A5:3799:G:H2'	69:A5:3800:G:C8	2.56	0.40
70:B2:522:G:H1'	70:B2:523:A:H5'	2.03	0.40
70:B2:581:C:C4	70:B2:582:G:H1'	2.56	0.40
70:B2:1382:G:H3'	70:B2:1383:A:C8	2.56	0.40
74:AF:94:ILE:HD12	74:AF:173:VAL:HG21	2.03	0.40
81:AS:10:GLN:NE2	81:AS:57:GLY:O	2.53	0.40
4:CM:21:LYS:HD2	25:Cf:38:LYS:HA	2.03	0.40
4:CM:43:THR:O	4:CM:43:THR:OG1	2.33	0.40
7:CI:97:ILE:HB	7:CI:124:GLY:HA3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CQ:80:ILE:HG23	9:CQ:139:LEU:HD12	2.03	0.40
10:CR:72:LYS:O	10:CR:74:ARG:NH1	2.55	0.40
12:CS:77:ASN:OD1	12:CS:98:ARG:NH1	2.51	0.40
13:CT:18:PRO:HB2	13:CT:21:LYS:HG3	2.03	0.40
13:CT:51:GLY:HA3	13:CT:92:ARG:HG3	2.02	0.40
21:CB:174:ARG:HD3	21:CB:174:ARG:HA	1.90	0.40
21:CB:261:ARG:HA	69:A5:2772:G:N3	2.37	0.40
22:CF:56:ARG:HE	22:CF:56:ARG:HB2	1.70	0.40
22:CF:231:TYR:HA	22:CF:236:ASP:H	1.86	0.40
29:CC:43:VAL:HG13	29:CC:118:VAL:HG11	2.03	0.40
43:AO:140:THR:OG1	43:AO:141:ARG:N	2.53	0.40
47:AN:107:LYS:HD2	47:AN:107:LYS:HA	1.83	0.40
48:AL:79:MET:HE3	48:AL:79:MET:HB2	1.83	0.40
61:AJ:176:ARG:HH22	70:B2:543:A:H5'	1.86	0.40
69:A5:286:A:H61	69:A5:313:A:H3'	1.87	0.40
69:A5:781:C:H2'	69:A5:782:G:C8	2.56	0.40
69:A5:1516:A:H4'	69:A5:1517:A:H5''	2.04	0.40
69:A5:3244:U:H2'	69:A5:3245:U:C5	2.56	0.40
69:A5:3587:U:H2'	69:A5:3588:G:C8	2.57	0.40
70:B2:279:G:N2	70:B2:288:C:O4'	2.54	0.40
70:B2:1194:C:H2'	70:B2:1195:G:H8	1.87	0.40
70:B2:1261:C:C5'	81:AS:130:ARG:CD	3.00	0.40
70:B2:1332:G:H22	70:B2:1338:U:H3	1.68	0.40
70:B2:1598:A:H5''	70:B2:1599:U:H5'	2.04	0.40
76:CU:257:LEU:HD23	76:CU:257:LEU:HA	1.96	0.40
76:CU:265:ASN:HB2	76:CU:267:LEU:HD13	2.03	0.40
79:Cg:44:CYS:HB3	79:Cg:47:CYS:HB2	2.03	0.40
2:CL:155:PRO:HG2	2:CL:157:LYS:HG2	2.04	0.40
5:Ca:13:ARG:HA	5:Ca:14:GLY:HA2	1.77	0.40
6:CN:165:THR:O	6:CN:169:LYS:HB2	2.20	0.40
9:CQ:5:ILE:HD12	9:CQ:5:ILE:HA	2.01	0.40
18:Cr:92:ARG:NH1	18:Cr:96:LYS:O	2.35	0.40
21:CB:128:LYS:O	21:CB:131:THR:OG1	2.37	0.40
26:Ci:35:ARG:HH11	69:A5:166:G:H5''	1.87	0.40
29:CC:16:LYS:HB2	29:CC:18:GLU:HG2	2.04	0.40
35:CH:103:THR:HG23	35:CH:110:ILE:HG13	2.03	0.40
41:Ag:41:ILE:HD12	41:Ag:59:ARG:HG3	2.02	0.40
41:Ag:59:ARG:NH1	67:AQ:104:GLU:OE1	2.49	0.40
51:AB:162:SER:OG	70:B2:961:U:OP1	2.36	0.40
55:AZ:47:VAL:CB	81:AS:23:LYS:O	2.67	0.40
55:AZ:49:PHE:H	81:AS:7:GLU:CG	2.30	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:AZ:82:LEU:HD23	55:AZ:85:ARG:HH11	1.87	0.40
59:Ae:111:ASN:O	59:Ae:115:VAL:N	2.55	0.40
61:AJ:79:LEU:H	61:AJ:79:LEU:HG	1.75	0.40
61:AJ:136:ILE:HD12	61:AJ:136:ILE:HA	1.85	0.40
64:AG:4:ASN:ND2	70:B2:149:U:O2	2.45	0.40
69:A5:637:U:H2'	69:A5:638:A:C8	2.57	0.40
69:A5:901:U:H3	69:A5:902:A:H62	1.68	0.40
69:A5:1326:A:H2'	69:A5:1327:G:C8	2.57	0.40
69:A5:1452:A:N6	69:A5:1468:U:O4	2.54	0.40
69:A5:3491:C:H2'	69:A5:3492:G:C8	2.55	0.40
69:A5:3762:G:O2'	69:A5:3766:U:O4'	2.36	0.40
70:B2:198:C:H2'	70:B2:199:G:H8	1.86	0.40
78:CW:57:ARG:HH11	78:CW:57:ARG:HD2	1.77	0.40
81:AS:58:GLU:HG3	81:AS:59:CYS:H	1.87	0.40
5:Ca:27:ARG:HD2	69:A5:1138:C:C5	2.57	0.40
6:CN:122:ALA:HB3	6:CN:129:TYR:CZ	2.56	0.40
6:CN:155:VAL:O	6:CN:162:ARG:NH2	2.44	0.40
6:CN:195:LYS:HD2	69:A5:103:A:H5'	2.04	0.40
8:CD:9:ASN:O	8:CD:11:GLN:N	2.54	0.40
8:CD:273:LEU:HG	39:A7:61:G:H5''	2.03	0.40
14:CP:4:TYR:OH	69:A5:407:A:OP1	2.27	0.40
14:CP:175:LEU:HD11	25:Cf:109:GLU:HG2	2.04	0.40
15:CX:161:ILE:N	69:A5:1813:A:O3'	2.50	0.40
16:CY:49:ILE:HD11	16:CY:55:VAL:HG21	2.03	0.40
17:CZ:12:ILE:HB	17:CZ:81:MET:HB3	2.04	0.40
23:Cc:21:VAL:HG13	23:Cc:25:GLY:HA3	2.04	0.40
26:Ci:35:ARG:NH1	69:A5:166:G:H5''	2.36	0.40
27:Ck:37:ARG:NH2	69:A5:1897:A:OP2	2.54	0.40
30:Cm:79:GLU:HA	30:Cm:80:PRO:HD3	1.91	0.40
33:Co:11:PHE:HE2	33:Co:13:LYS:HB3	1.86	0.40
33:Co:33:LYS:HA	33:Co:34:GLY:HA2	1.62	0.40
36:CE:208:ALA:O	36:CE:211:LYS:NZ	2.37	0.40
52:AA:85:ARG:HG2	52:AA:89:LYS:HZ1	1.87	0.40
57:Ab:35:VAL:HA	57:Ab:79:PHE:HA	2.02	0.40
69:A5:262:G:N2	69:A5:263:A:H62	2.19	0.40
69:A5:578:A:H1'	69:A5:633:A:C2	2.57	0.40
69:A5:1796:A:C8	69:A5:1797:A:C8	3.10	0.40
69:A5:2902:C:H2'	69:A5:2903:U:C6	2.57	0.40
69:A5:3592:C:P	69:A5:3593:A:H5''	2.62	0.40
70:B2:1445:A:H4'	72:AT:129:ARG:HH11	1.86	0.40
70:B2:1465:U:N3	70:B2:1525:A:N1	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:B2:1696:G:H5'	72:AT:41:LYS:HZ2	1.86	0.40
70:B2:1795:U:H2'	70:B2:1796:C:H6	1.86	0.40
73:AK:22:VAL:O	73:AK:40:ASN:ND2	2.54	0.40
73:AK:25:LYS:HE2	73:AK:25:LYS:HB2	1.73	0.40
74:AF:54:ILE:HD13	74:AF:135:LEU:HD12	2.03	0.40
74:AF:156:ARG:NH1	75:Ac:19:SER:O	2.55	0.40
74:AF:190:ARG:HD2	74:AF:190:ARG:HA	1.90	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CO	203/205 (99%)	177 (87%)	24 (12%)	2 (1%)	12	45
2	CL	208/210 (99%)	154 (74%)	42 (20%)	12 (6%)	1	8
3	CV	132/134 (98%)	122 (92%)	10 (8%)	0	100	100
4	CM	157/159 (99%)	129 (82%)	27 (17%)	1 (1%)	21	56
5	Ca	147/149 (99%)	113 (77%)	33 (22%)	1 (1%)	18	53
6	CN	201/203 (99%)	166 (83%)	32 (16%)	3 (2%)	8	35
7	CI	215/217 (99%)	183 (85%)	30 (14%)	2 (1%)	14	48
8	CD	288/290 (99%)	247 (86%)	39 (14%)	2 (1%)	18	53
9	CQ	185/187 (99%)	160 (86%)	25 (14%)	0	100	100
10	CR	201/203 (99%)	183 (91%)	18 (9%)	0	100	100
11	CA	251/253 (99%)	211 (84%)	39 (16%)	1 (0%)	30	65
12	CS	171/173 (99%)	126 (74%)	37 (22%)	8 (5%)	2	11
13	CT	156/158 (99%)	130 (83%)	25 (16%)	1 (1%)	21	56
14	CP	183/185 (99%)	163 (89%)	19 (10%)	1 (0%)	24	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	CX	118/120 (98%)	98 (83%)	19 (16%)	1 (1%)	16	50
16	CY	129/131 (98%)	112 (87%)	16 (12%)	1 (1%)	16	50
17	CZ	132/134 (98%)	110 (83%)	21 (16%)	1 (1%)	16	50
18	Cr	132/134 (98%)	81 (61%)	47 (36%)	4 (3%)	3	19
19	Ch	121/123 (98%)	106 (88%)	15 (12%)	0	100	100
20	Cb	73/75 (97%)	59 (81%)	11 (15%)	3 (4%)	2	13
21	CB	412/414 (100%)	346 (84%)	56 (14%)	10 (2%)	4	24
22	CF	224/226 (99%)	199 (89%)	20 (9%)	5 (2%)	5	26
23	Cc	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
24	Ce	130/132 (98%)	118 (91%)	11 (8%)	1 (1%)	16	50
25	Cf	155/157 (99%)	113 (73%)	36 (23%)	6 (4%)	2	14
26	Ci	111/113 (98%)	82 (74%)	28 (25%)	1 (1%)	14	48
27	Ck	68/70 (97%)	61 (90%)	7 (10%)	0	100	100
28	Cl	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
29	CC	390/392 (100%)	318 (82%)	67 (17%)	5 (1%)	9	38
30	Cm	50/52 (96%)	43 (86%)	6 (12%)	1 (2%)	6	28
31	Cn	23/25 (92%)	21 (91%)	2 (9%)	0	100	100
32	Cp	89/91 (98%)	80 (90%)	9 (10%)	0	100	100
33	Co	102/104 (98%)	82 (80%)	18 (18%)	2 (2%)	6	28
34	CJ	180/182 (99%)	149 (83%)	30 (17%)	1 (1%)	21	56
35	CH	188/190 (99%)	164 (87%)	21 (11%)	3 (2%)	7	34
36	CE	226/228 (99%)	157 (70%)	62 (27%)	7 (3%)	3	19
37	CG	239/241 (99%)	194 (81%)	43 (18%)	2 (1%)	16	50
41	Ag	316/318 (99%)	265 (84%)	51 (16%)	0	100	100
42	AU	100/102 (98%)	89 (89%)	11 (11%)	0	100	100
43	AO	125/127 (98%)	100 (80%)	25 (20%)	0	100	100
44	AX	141/143 (99%)	120 (85%)	20 (14%)	1 (1%)	18	53
45	AM	117/119 (98%)	85 (73%)	32 (27%)	0	100	100
46	Ad	50/52 (96%)	33 (66%)	17 (34%)	0	100	100
47	AN	148/150 (99%)	137 (93%)	11 (7%)	0	100	100
48	AL	153/155 (99%)	133 (87%)	19 (12%)	1 (1%)	18	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	AR	118/120 (98%)	92 (78%)	25 (21%)	1 (1%)	16	50
50	AP	122/124 (98%)	96 (79%)	26 (21%)	0	100	100
51	AB	218/220 (99%)	176 (81%)	37 (17%)	5 (2%)	5	25
52	AA	216/218 (99%)	179 (83%)	36 (17%)	1 (0%)	24	60
53	AV	80/82 (98%)	67 (84%)	13 (16%)	0	100	100
54	AY	124/126 (98%)	101 (82%)	22 (18%)	1 (1%)	16	50
55	AZ	72/74 (97%)	56 (78%)	16 (22%)	0	100	100
56	Aa	105/107 (98%)	86 (82%)	18 (17%)	1 (1%)	12	45
57	Ab	82/84 (98%)	64 (78%)	18 (22%)	0	100	100
58	AD	225/227 (99%)	179 (80%)	44 (20%)	2 (1%)	14	48
59	Ae	56/58 (97%)	39 (70%)	17 (30%)	0	100	100
60	Af	78/80 (98%)	57 (73%)	21 (27%)	0	100	100
61	AJ	179/181 (99%)	152 (85%)	26 (14%)	1 (1%)	21	56
62	AE	259/261 (99%)	215 (83%)	42 (16%)	2 (1%)	16	50
63	AC	225/227 (99%)	188 (84%)	35 (16%)	2 (1%)	14	48
64	AG	229/231 (99%)	197 (86%)	30 (13%)	2 (1%)	14	48
65	AH	192/194 (99%)	161 (84%)	31 (16%)	0	100	100
66	AI	205/207 (99%)	161 (78%)	41 (20%)	3 (2%)	8	35
67	AQ	146/148 (99%)	116 (80%)	29 (20%)	1 (1%)	18	53
68	Cz	215/217 (99%)	175 (81%)	40 (19%)	0	100	100
71	AW	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
72	AT	122/126 (97%)	92 (75%)	29 (24%)	1 (1%)	16	50
73	AK	88/90 (98%)	64 (73%)	24 (27%)	0	100	100
74	AF	187/189 (99%)	146 (78%)	41 (22%)	0	100	100
75	Ac	60/62 (97%)	49 (82%)	11 (18%)	0	100	100
76	CU	97/99 (98%)	73 (75%)	23 (24%)	1 (1%)	12	45
77	Cj	85/87 (98%)	74 (87%)	10 (12%)	1 (1%)	10	40
78	CW	58/60 (97%)	53 (91%)	5 (9%)	0	100	100
79	Cg	101/103 (98%)	90 (89%)	10 (10%)	1 (1%)	12	45
80	Cd	105/107 (98%)	97 (92%)	8 (8%)	0	100	100
81	AS	134/136 (98%)	117 (87%)	16 (12%)	1 (1%)	18	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	11596/11750 (99%)	9587 (83%)	1892 (16%)	117 (1%)	15	45

All (117) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	CO	112	SER
1	CO	113	PRO
2	CL	7	MET
2	CL	148	GLN
2	CL	160	GLN
8	CD	20	PHE
21	CB	19	LYS
21	CB	41	VAL
22	CF	171	PRO
22	CF	236	ASP
22	CF	237	PHE
26	Ci	44	THR
29	CC	6	ALA
34	CJ	97	TYR
36	CE	69	TYR
51	AB	120	TRP
51	AB	183	ASP
51	AB	184	LEU
66	AI	99	ASN
2	CL	46	PHE
2	CL	76	THR
2	CL	77	LEU
2	CL	97	VAL
5	Ca	79	LEU
12	CS	54	PHE
12	CS	68	TYR
12	CS	119	ALA
12	CS	133	PRO
12	CS	174	THR
13	CT	5	LYS
16	CY	63	LYS
21	CB	40	PRO
21	CB	64	GLY
21	CB	271	GLN
21	CB	394	LYS
21	CB	395	ASP
22	CF	100	GLY

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Mol	Chain	Res	Type
24	Ce	15	ARG
29	CC	92	GLN
33	Co	27	LYS
35	CH	110	ILE
36	CE	24	SER
51	AB	119	LYS
52	AA	32	PHE
76	CU	279	ASP
2	CL	125	LEU
2	CL	161	PRO
4	CM	104	LEU
6	CN	149	ASN
11	CA	231	ALA
12	CS	139	ARG
17	CZ	97	PRO
18	Cr	70	LYS
18	Cr	82	VAL
20	Cb	7	HIS
20	Cb	24	PRO
29	CC	313	PHE
35	CH	23	ARG
37	CG	44	PHE
66	AI	141	LYS
79	Cg	73	SER
2	CL	159	GLU
7	CI	205	PRO
20	Cb	4	SER
21	CB	312	LYS
25	Cf	21	PRO
25	Cf	138	ASN
29	CC	204	ARG
36	CE	60	VAL
56	Aa	100	ARG
58	AD	202	PRO
62	AE	241	GLY
63	AC	242	MET
64	AG	149	LYS
67	AQ	46	PRO
77	Cj	86	PRO
2	CL	152	PRO
6	CN	187	SER
8	CD	221	ARG

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Mol	Chain	Res	Type
12	CS	171	LYS
14	CP	21	ASN
25	Cf	38	LYS
30	Cm	125	LYS
36	CE	61	PRO
36	CE	193	VAL
44	AX	96	GLU
48	AL	28	LYS
51	AB	41	THR
54	AY	6	ALA
64	AG	100	CYS
66	AI	143	ARG
6	CN	188	ARG
15	CX	227	LYS
21	CB	190	ILE
25	Cf	108	PRO
33	Co	30	LYS
35	CH	109	VAL
36	CE	89	ARG
12	CS	152	PHE
18	Cr	71	GLY
49	AR	45	PRO
72	AT	86	GLY
81	AS	140	GLY
21	CB	39	LYS
22	CF	172	ILE
29	CC	93	GLY
58	AD	200	ILE
63	AC	159	LYS
2	CL	61	PRO
25	Cf	139	LEU
36	CE	70	PRO
61	AJ	7	PRO
25	Cf	107	HIS
62	AE	239	PRO
7	CI	206	ILE
37	CG	168	PRO
18	Cr	77	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CO	175/175 (100%)	173 (99%)	2 (1%)	65	83
2	CL	173/173 (100%)	167 (96%)	6 (4%)	32	65
3	CV	101/101 (100%)	101 (100%)	0	100	100
4	CM	138/138 (100%)	137 (99%)	1 (1%)	76	86
5	Ca	122/122 (100%)	120 (98%)	2 (2%)	55	79
6	CN	174/174 (100%)	168 (97%)	6 (3%)	32	66
7	CI	187/187 (100%)	186 (100%)	1 (0%)	81	89
8	CD	241/241 (100%)	240 (100%)	1 (0%)	84	90
9	CQ	164/164 (100%)	160 (98%)	4 (2%)	43	73
10	CR	176/176 (100%)	175 (99%)	1 (1%)	78	88
11	CA	195/195 (100%)	193 (99%)	2 (1%)	68	84
12	CS	156/156 (100%)	152 (97%)	4 (3%)	40	72
13	CT	137/137 (100%)	135 (98%)	2 (2%)	57	80
14	CP	160/160 (100%)	151 (94%)	9 (6%)	19	52
15	CX	106/106 (100%)	105 (99%)	1 (1%)	70	85
16	CY	116/116 (100%)	111 (96%)	5 (4%)	26	60
17	CZ	121/121 (100%)	121 (100%)	0	100	100
18	Cr	112/112 (100%)	111 (99%)	1 (1%)	70	85
19	Ch	112/112 (100%)	110 (98%)	2 (2%)	51	77
20	Cb	67/67 (100%)	66 (98%)	1 (2%)	57	80
21	CB	349/349 (100%)	341 (98%)	8 (2%)	44	74
22	CF	200/200 (100%)	197 (98%)	3 (2%)	57	80
23	Cc	84/84 (100%)	84 (100%)	0	100	100
24	Ce	120/120 (100%)	119 (99%)	1 (1%)	73	86
25	Cf	123/123 (100%)	121 (98%)	2 (2%)	55	79
26	Ci	100/100 (100%)	98 (98%)	2 (2%)	48	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	Ck	65/65 (100%)	63 (97%)	2 (3%)	35	68
28	Cl	45/45 (100%)	45 (100%)	0	100	100
29	CC	323/323 (100%)	317 (98%)	6 (2%)	50	76
30	Cm	48/48 (100%)	45 (94%)	3 (6%)	16	48
31	Cn	23/23 (100%)	23 (100%)	0	100	100
32	Cp	74/74 (100%)	69 (93%)	5 (7%)	14	45
33	Co	94/94 (100%)	93 (99%)	1 (1%)	65	83
34	CJ	155/155 (100%)	151 (97%)	4 (3%)	40	72
35	CH	169/169 (100%)	165 (98%)	4 (2%)	43	73
36	CE	197/197 (100%)	189 (96%)	8 (4%)	27	61
37	CG	210/210 (100%)	205 (98%)	5 (2%)	43	73
41	Ag	280/280 (100%)	276 (99%)	4 (1%)	59	80
42	AU	95/95 (100%)	94 (99%)	1 (1%)	65	83
43	AO	98/98 (100%)	96 (98%)	2 (2%)	48	76
44	AX	116/116 (100%)	115 (99%)	1 (1%)	70	85
45	AM	104/104 (100%)	100 (96%)	4 (4%)	29	63
46	Ad	45/45 (100%)	45 (100%)	0	100	100
47	AN	130/130 (100%)	130 (100%)	0	100	100
48	AL	138/138 (100%)	135 (98%)	3 (2%)	45	74
49	AR	108/108 (100%)	106 (98%)	2 (2%)	50	76
50	AP	111/111 (100%)	111 (100%)	0	100	100
51	AB	199/199 (100%)	198 (100%)	1 (0%)	81	89
52	AA	190/190 (100%)	189 (100%)	1 (0%)	81	89
53	AV	67/67 (100%)	66 (98%)	1 (2%)	57	80
54	AY	105/106 (99%)	103 (98%)	2 (2%)	50	76
55	AZ	67/67 (100%)	64 (96%)	3 (4%)	24	59
56	Aa	94/94 (100%)	92 (98%)	2 (2%)	47	75
57	Ab	72/72 (100%)	72 (100%)	0	100	100
58	AD	192/192 (100%)	191 (100%)	1 (0%)	81	89
59	Ae	47/47 (100%)	47 (100%)	0	100	100
60	Af	70/70 (100%)	69 (99%)	1 (1%)	59	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
61	AJ	161/161 (100%)	161 (100%)	0	100	100
62	AE	220/220 (100%)	218 (99%)	2 (1%)	70	85
63	AC	188/188 (100%)	187 (100%)	1 (0%)	81	89
64	AG	200/200 (100%)	198 (99%)	2 (1%)	68	84
65	AH	175/175 (100%)	173 (99%)	2 (1%)	65	83
66	AI	175/175 (100%)	174 (99%)	1 (1%)	78	88
67	AQ	122/122 (100%)	121 (99%)	1 (1%)	73	86
68	Cz	190/190 (100%)	189 (100%)	1 (0%)	81	89
71	AW	113/113 (100%)	111 (98%)	2 (2%)	51	77
72	AT	104/104 (100%)	102 (98%)	2 (2%)	50	76
73	AK	81/81 (100%)	79 (98%)	2 (2%)	42	72
74	AF	157/157 (100%)	151 (96%)	6 (4%)	29	63
75	Ac	54/54 (100%)	52 (96%)	2 (4%)	30	64
76	CU	92/92 (100%)	90 (98%)	2 (2%)	45	74
77	Cj	74/74 (100%)	72 (97%)	2 (3%)	39	71
78	CW	54/54 (100%)	53 (98%)	1 (2%)	50	76
79	Cg	95/95 (100%)	87 (92%)	8 (8%)	10	37
80	Cd	99/99 (100%)	86 (87%)	13 (13%)	4	19
81	AS	122/122 (100%)	122 (100%)	0	100	100
All	All	10116/10117 (100%)	9932 (98%)	184 (2%)	51	77

All (184) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	CO	24	VAL
1	CO	35	VAL
2	CL	8	ILE
2	CL	58	VAL
2	CL	125	LEU
2	CL	137	GLU
2	CL	164	VAL
2	CL	192	VAL
4	CM	54	ASN
5	Ca	4	ILE
5	Ca	144	VAL

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Mol	Chain	Res	Type
6	CN	23	LEU
6	CN	34	THR
6	CN	64	ILE
6	CN	80	THR
6	CN	134	LEU
6	CN	155	VAL
7	CI	203	HIS
8	CD	155	THR
9	CQ	85	THR
9	CQ	156	PRO
9	CQ	163	THR
9	CQ	167	VAL
10	CR	47	ASP
11	CA	177	LYS
11	CA	191	VAL
12	CS	17	LEU
12	CS	150	ILE
12	CS	155	VAL
12	CS	174	THR
13	CT	67	VAL
13	CT	80	VAL
14	CP	24	VAL
14	CP	29	THR
14	CP	57	CYS
14	CP	82	ARG
14	CP	116	HIS
14	CP	119	VAL
14	CP	129	THR
14	CP	146	VAL
14	CP	148	VAL
15	CX	186	VAL
16	CY	55	VAL
16	CY	70	VAL
16	CY	79	VAL
16	CY	104	VAL
16	CY	107	VAL
18	Cr	106	TYR
19	Ch	58	TYR
19	Ch	122	LYS
20	Cb	43	GLN
21	CB	1	MET
21	CB	103	VAL

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Mol	Chain	Res	Type
21	CB	207	VAL
21	CB	218	ASP
21	CB	232	THR
21	CB	268	ARG
21	CB	323	TYR
21	CB	338	ILE
22	CF	92	LEU
22	CF	143	ILE
22	CF	163	VAL
24	Ce	2	THR
25	Cf	95	VAL
25	Cf	131	VAL
26	Ci	3	VAL
26	Ci	9	ILE
27	Ck	47	VAL
27	Ck	66	VAL
29	CC	30	VAL
29	CC	45	GLN
29	CC	235	VAL
29	CC	323	THR
29	CC	324	ASN
29	CC	327	GLN
30	Cm	103	LEU
30	Cm	119	ASN
30	Cm	120	ASN
32	Cp	16	THR
32	Cp	51	VAL
32	Cp	52	VAL
32	Cp	54	ILE
32	Cp	63	THR
33	Co	4	VAL
34	CJ	44	VAL
34	CJ	138	VAL
34	CJ	146	VAL
34	CJ	162	LEU
35	CH	3	THR
35	CH	20	VAL
35	CH	102	VAL
35	CH	165	VAL
36	CE	26	LEU
36	CE	55	VAL
36	CE	71	THR

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Mol	Chain	Res	Type
36	CE	73	THR
36	CE	79	PRO
36	CE	95	LEU
36	CE	145	VAL
36	CE	193	VAL
37	CG	81	VAL
37	CG	132	VAL
37	CG	171	LEU
37	CG	172	VAL
37	CG	219	ASN
41	Ag	6	GLN
41	Ag	143	ILE
41	Ag	179	ASN
41	Ag	271	LEU
42	AU	52	VAL
43	AO	47	LEU
43	AO	103	ASN
44	AX	39	ASN
45	AM	22	ASN
45	AM	58	ILE
45	AM	84	ILE
45	AM	130	VAL
48	AL	31	LEU
48	AL	37	VAL
48	AL	71	THR
49	AR	66	VAL
49	AR	85	VAL
51	AB	128	VAL
52	AA	191	ARG
53	AV	69	ILE
54	AY	51	VAL
54	AY	103	GLN
55	AZ	61	VAL
55	AZ	72	VAL
55	AZ	112	THR
56	Aa	11	ASN
56	Aa	13	HIS
58	AD	177	VAL
60	Af	149	VAL
62	AE	9	LEU
62	AE	136	VAL
63	AC	163	VAL

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Mol	Chain	Res	Type
64	AG	67	VAL
64	AG	158	VAL
65	AH	93	ILE
65	AH	132	VAL
66	AI	140	THR
67	AQ	72	VAL
68	Cz	82	VAL
71	AW	35	ILE
71	AW	105	THR
72	AT	22	LEU
72	AT	30	VAL
73	AK	9	VAL
73	AK	81	LEU
74	AF	54	ILE
74	AF	64	TYR
74	AF	65	ILE
74	AF	125	ILE
74	AF	129	LEU
74	AF	201	ASP
75	Ac	37	GLN
75	Ac	52	LEU
76	CU	225	VAL
76	CU	277	GLU
77	Cj	68	LYS
77	Cj	70	VAL
78	CW	52	THR
79	Cg	2	VAL
79	Cg	3	GLN
79	Cg	22	ILE
79	Cg	25	THR
79	Cg	32	TYR
79	Cg	33	GLN
79	Cg	58	ARG
79	Cg	75	THR
80	Cd	17	VAL
80	Cd	18	VAL
80	Cd	19	THR
80	Cd	24	ILE
80	Cd	30	VAL
80	Cd	33	ILE
80	Cd	65	LEU
80	Cd	83	VAL

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Mol	Chain	Res	Type
80	Cd	91	ASP
80	Cd	92	ASP
80	Cd	101	THR
80	Cd	104	THR
80	Cd	119	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (107) such sidechains are listed below:

Mol	Chain	Res	Type
2	CL	11	GLN
2	CL	110	GLN
2	CL	148	GLN
4	CM	97	ASN
6	CN	37	HIS
6	CN	182	GLN
7	CI	14	ASN
7	CI	73	ASN
8	CD	11	GLN
8	CD	269	ASN
9	CQ	7	HIS
9	CQ	64	GLN
9	CQ	125	GLN
9	CQ	135	ASN
12	CS	177	GLN
13	CT	134	GLN
14	CP	30	HIS
14	CP	75	GLN
14	CP	115	HIS
15	CX	196	ASN
15	CX	272	ASN
16	CY	20	GLN
17	CZ	29	HIS
17	CZ	78	ASN
17	CZ	126	ASN
18	Cr	99	ASN
19	Ch	68	ASN
20	Cb	19	ASN
20	Cb	43	GLN
20	Cb	61	ASN
21	CB	25	HIS
21	CB	148	ASN
21	CB	245	HIS

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Mol	Chain	Res	Type
22	CF	129	ASN
22	CF	229	ASN
23	Cc	78	ASN
24	Ce	51	GLN
26	Ci	15	HIS
29	CC	320	ASN
29	CC	327	GLN
33	Co	45	GLN
33	Co	51	GLN
34	CJ	47	GLN
35	CH	134	ASN
35	CH	138	GLN
36	CE	94	ASN
36	CE	195	ASN
36	CE	202	GLN
37	CG	71	GLN
41	Ag	24	ASN
41	Ag	52	ASN
41	Ag	57	GLN
41	Ag	77	ASN
41	Ag	118	ASN
41	Ag	144	GLN
41	Ag	179	ASN
41	Ag	188	ASN
41	Ag	238	ASN
41	Ag	284	GLN
45	AM	80	GLN
45	AM	137	GLN
45	AM	138	ASN
46	Ad	26	ASN
46	Ad	28	HIS
46	Ad	37	ASN
48	AL	10	GLN
48	AL	91	HIS
48	AL	146	GLN
49	AR	113	ASN
51	AB	75	GLN
51	AB	95	GLN
51	AB	151	GLN
51	AB	211	HIS
54	AY	37	ASN
55	AZ	46	GLN

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Mol	Chain	Res	Type
55	AZ	105	GLN
56	Aa	80	HIS
58	AD	76	GLN
58	AD	176	HIS
60	Af	115	HIS
61	AJ	141	GLN
62	AE	8	HIS
63	AC	116	ASN
64	AG	187	GLN
66	AI	52	ASN
66	AI	64	ASN
66	AI	155	GLN
67	AQ	99	GLN
67	AQ	116	GLN
68	Cz	96	ASN
68	Cz	181	GLN
71	AW	5	ASN
71	AW	15	ASN
72	AT	66	HIS
72	AT	91	HIS
72	AT	105	GLN
73	AK	42	HIS
74	AF	121	HIS
74	AF	133	ASN
75	Ac	34	GLN
77	Cj	36	GLN
79	Cg	3	GLN
80	Cd	90	ASN
81	AS	10	GLN
81	AS	73	ASN
81	AS	120	HIS
81	AS	135	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
38	A9	29/30 (96%)	8 (27%)	1 (3%)
39	A7	119/120 (99%)	30 (25%)	1 (0%)
40	A8	122/123 (99%)	45 (36%)	1 (0%)
69	A5	3555/3703 (96%)	1353 (38%)	81 (2%)
70	B2	1788/1936 (92%)	627 (35%)	32 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	5613/5912 (94%)	2063 (36%)	116 (2%)

All (2063) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
38	A9	4	U
38	A9	9	C
38	A9	20	U
38	A9	21	G
38	A9	22	A
38	A9	25	G
38	A9	26	U
38	A9	30	A
39	A7	7	G
39	A7	17	C
39	A7	22	A
39	A7	25	A
39	A7	27	A
39	A7	33	U
39	A7	39	C
39	A7	40	C
39	A7	41	G
39	A7	42	A
39	A7	47	C
39	A7	50	A
39	A7	52	U
39	A7	53	U
39	A7	54	A
39	A7	58	A
39	A7	60	C
39	A7	64	G
39	A7	70	G
39	A7	74	A
39	A7	89	G
39	A7	90	A
39	A7	93	G
39	A7	97	G
39	A7	100	A
39	A7	108	G
39	A7	109	U
39	A7	110	G
39	A7	117	G

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Mol	Chain	Res	Type
39	A7	120	U
40	A8	2	A
40	A8	6	U
40	A8	13	U
40	A8	15	G
40	A8	20	C
40	A8	22	C
40	A8	23	G
40	A8	32	G
40	A8	33	U
40	A8	34	C
40	A8	37	U
40	A8	38	G
40	A8	45	G
40	A8	47	A
40	A8	50	A
40	A8	56	U
40	A8	57	G
40	A8	59	G
40	A8	61	C
40	A8	62	A
40	A8	70	A
40	A8	73	U
40	A8	74	G
40	A8	75	C
40	A8	78	G
40	A8	79	A
40	A8	80	C
40	A8	81	A
40	A8	82	C
40	A8	83	A
40	A8	84	U
40	A8	89	A
40	A8	92	G
40	A8	94	C
40	A8	97	U
40	A8	102	A
40	A8	103	C
40	A8	109	U
40	A8	110	C
40	A8	111	G
40	A8	113	A

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Mol	Chain	Res	Type
40	A8	118	A
40	A8	119	U
40	A8	122	U
40	A8	123	G
69	A5	2	U
69	A5	3	A
69	A5	4	U
69	A5	6	U
69	A5	7	A
69	A5	9	A
69	A5	11	C
69	A5	13	U
69	A5	14	C
69	A5	15	A
69	A5	17	C
69	A5	18	U
69	A5	19	C
69	A5	22	A
69	A5	23	U
69	A5	25	G
69	A5	26	G
69	A5	29	U
69	A5	30	A
69	A5	35	C
69	A5	36	U
69	A5	44	A
69	A5	45	G
69	A5	46	C
69	A5	47	A
69	A5	48	U
69	A5	53	A
69	A5	54	U
69	A5	59	G
69	A5	61	A
69	A5	62	G
69	A5	63	G
69	A5	64	A
69	A5	69	A
69	A5	70	A
69	A5	72	C
69	A5	73	U
69	A5	77	A

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Mol	Chain	Res	Type
69	A5	78	A
69	A5	79	G
69	A5	80	G
69	A5	82	U
69	A5	90	G
69	A5	94	C
69	A5	96	G
69	A5	98	G
69	A5	103	A
69	A5	110	A
69	A5	112	C
69	A5	113	A
69	A5	114	G
69	A5	117	C
69	A5	121	A
69	A5	122	C
69	A5	123	U
69	A5	124	A
69	A5	125	A
69	A5	127	U
69	A5	128	C
69	A5	136	C
69	A5	137	U
69	A5	138	A
69	A5	139	U
69	A5	141	U
69	A5	142	G
69	A5	148	U
69	A5	149	G
69	A5	154	A
69	A5	156	G
69	A5	157	C
69	A5	158	A
69	A5	162	U
69	A5	163	A
69	A5	164	U
69	A5	165	G
69	A5	166	G
69	A5	169	C
69	A5	171	U
69	A5	174	A
69	A5	175	U

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Mol	Chain	Res	Type
69	A5	176	A
69	A5	178	U
69	A5	182	G
69	A5	183	U
69	A5	187	A
69	A5	188	G
69	A5	189	A
69	A5	190	A
69	A5	191	A
69	A5	197	G
69	A5	198	A
69	A5	199	U
69	A5	201	U
69	A5	202	A
69	A5	205	U
69	A5	206	C
69	A5	207	C
69	A5	209	U
69	A5	210	C
69	A5	212	U
69	A5	213	A
69	A5	216	U
69	A5	225	U
69	A5	226	U
69	A5	227	A
69	A5	228	C
69	A5	229	C
69	A5	232	U
69	A5	233	A
69	A5	240	G
69	A5	241	C
69	A5	242	C
69	A5	244	G
69	A5	253	A
69	A5	261	U
69	A5	262	G
69	A5	269	A
69	A5	272	U
69	A5	273	G
69	A5	274	A
69	A5	276	G
69	A5	277	U

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Mol	Chain	Res	Type
69	A5	279	U
69	A5	285	G
69	A5	287	G
69	A5	288	U
69	A5	289	C
69	A5	294	U
69	A5	297	U
69	A5	298	U
69	A5	301	U
69	A5	302	A
69	A5	303	G
69	A5	304	U
69	A5	308	G
69	A5	313	A
69	A5	316	U
69	A5	317	G
69	A5	323	U
69	A5	329	C
69	A5	333	C
69	A5	335	A
69	A5	341	A
69	A5	347	A
69	A5	354	A
69	A5	355	G
69	A5	367	A
69	A5	368	C
69	A5	370	A
69	A5	388	U
69	A5	394	G
69	A5	396	A
69	A5	405	A
69	A5	409	A
69	A5	413	A
69	A5	415	A
69	A5	416	C
69	A5	417	A
69	A5	420	A
69	A5	421	C
69	A5	422	G
69	A5	425	A
69	A5	428	C
69	A5	429	U

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Mol	Chain	Res	Type
69	A5	430	G
69	A5	439	U
69	A5	440	U
69	A5	441	A
69	A5	445	C
69	A5	446	C
69	A5	458	A
69	A5	459	U
69	A5	460	A
69	A5	461	U
69	A5	462	C
69	A5	463	C
69	A5	464	G
69	A5	465	U
69	A5	466	U
69	A5	467	A
69	A5	468	U
69	A5	475	U
69	A5	476	U
69	A5	478	A
69	A5	479	U
69	A5	483	U
69	A5	495	A
69	A5	499	A
69	A5	500	A
69	A5	508	U
69	A5	509	A
69	A5	519	U
69	A5	520	G
69	A5	521	U
69	A5	522	G
69	A5	523	C
69	A5	524	A
69	A5	525	U
69	A5	526	U
69	A5	527	U
69	A5	533	A
69	A5	534	U
69	A5	535	A
69	A5	536	U
69	A5	537	A
69	A5	539	G

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Mol	Chain	Res	Type
69	A5	540	G
69	A5	541	A
69	A5	548	A
69	A5	555	U
69	A5	558	C
69	A5	559	A
69	A5	560	U
69	A5	566	A
69	A5	567	A
69	A5	568	A
69	A5	569	U
69	A5	571	U
69	A5	576	U
69	A5	577	A
69	A5	578	A
69	A5	580	A
69	A5	581	U
69	A5	582	A
69	A5	585	A
69	A5	586	C
69	A5	588	U
69	A5	590	U
69	A5	592	G
69	A5	593	U
69	A5	616	A
69	A5	618	U
69	A5	620	U
69	A5	621	A
69	A5	622	A
69	A5	623	C
69	A5	625	C
69	A5	629	A
69	A5	630	U
69	A5	631	A
69	A5	632	A
69	A5	633	A
69	A5	634	U
69	A5	635	G
69	A5	636	U
69	A5	637	U
69	A5	640	U
69	A5	641	A

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Mol	Chain	Res	Type
69	A5	642	A
69	A5	643	U
69	A5	646	G
69	A5	652	G
69	A5	653	U
69	A5	659	U
69	A5	665	U
69	A5	666	A
69	A5	667	U
69	A5	668	A
69	A5	669	U
69	A5	670	G
69	A5	671	A
69	A5	672	U
69	A5	673	U
69	A5	674	A
69	A5	679	G
69	A5	680	C
69	A5	681	G
69	A5	682	U
69	A5	683	U
69	A5	689	U
69	A5	690	U
69	A5	692	G
69	A5	693	G
69	A5	711	A
69	A5	717	A
69	A5	719	U
69	A5	726	U
69	A5	729	G
69	A5	731	U
69	A5	732	U
69	A5	745	U
69	A5	746	G
69	A5	747	U
69	A5	748	A
69	A5	749	U
69	A5	750	G
69	A5	751	A
69	A5	752	U
69	A5	753	U
69	A5	754	A

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Mol	Chain	Res	Type
69	A5	755	A
69	A5	761	C
69	A5	762	G
69	A5	763	A
69	A5	764	A
69	A5	765	A
69	A5	766	G
69	A5	767	A
69	A5	774	A
69	A5	775	U
69	A5	776	A
69	A5	777	C
69	A5	783	G
69	A5	786	C
69	A5	789	G
69	A5	797	A
69	A5	799	A
69	A5	806	A
69	A5	810	A
69	A5	812	U
69	A5	824	G
69	A5	827	A
69	A5	831	A
69	A5	832	U
69	A5	833	U
69	A5	834	G
69	A5	838	U
69	A5	840	U
69	A5	841	A
69	A5	858	U
69	A5	862	U
69	A5	863	U
69	A5	865	A
69	A5	866	C
69	A5	868	A
69	A5	869	A
69	A5	870	U
69	A5	872	A
69	A5	873	U
69	A5	874	G
69	A5	879	U
69	A5	880	A

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Mol	Chain	Res	Type
69	A5	883	U
69	A5	884	U
69	A5	885	U
69	A5	887	U
69	A5	888	A
69	A5	891	U
69	A5	892	A
69	A5	893	U
69	A5	894	U
69	A5	895	U
69	A5	896	A
69	A5	898	A
69	A5	899	G
69	A5	901	U
69	A5	905	U
69	A5	909	A
69	A5	913	U
69	A5	917	G
69	A5	921	C
69	A5	922	G
69	A5	926	U
69	A5	927	A
69	A5	928	U
69	A5	929	A
69	A5	930	U
69	A5	932	G
69	A5	933	U
69	A5	936	U
69	A5	937	G
69	A5	942	A
69	A5	963	G
69	A5	964	C
69	A5	968	U
69	A5	969	A
69	A5	975	A
69	A5	981	C
69	A5	984	U
69	A5	985	G
69	A5	992	U
69	A5	998	G
69	A5	1001	A
69	A5	1005	G

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Mol	Chain	Res	Type
69	A5	1006	A
69	A5	1007	A
69	A5	1008	A
69	A5	1009	G
69	A5	1010	A
69	A5	1016	A
69	A5	1017	A
69	A5	1028	U
69	A5	1030	A
69	A5	1032	G
69	A5	1043	G
69	A5	1049	C
69	A5	1053	G
69	A5	1054	A
69	A5	1057	G
69	A5	1058	A
69	A5	1061	A
69	A5	1064	G
69	A5	1069	A
69	A5	1071	U
69	A5	1074	U
69	A5	1079	U
69	A5	1080	G
69	A5	1084	A
69	A5	1087	G
69	A5	1089	U
69	A5	1094	A
69	A5	1096	A
69	A5	1097	A
69	A5	1101	A
69	A5	1107	G
69	A5	1108	G
69	A5	1114	A
69	A5	1116	G
69	A5	1117	A
69	A5	1118	C
69	A5	1120	A
69	A5	1121	A
69	A5	1123	C
69	A5	1124	G
69	A5	1126	A
69	A5	1132	U

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Mol	Chain	Res	Type
69	A5	1137	G
69	A5	1138	C
69	A5	1144	C
69	A5	1145	C
69	A5	1159	C
69	A5	1160	U
69	A5	1162	A
69	A5	1163	G
69	A5	1183	U
69	A5	1193	A
69	A5	1194	A
69	A5	1195	U
69	A5	1197	A
69	A5	1198	U
69	A5	1199	C
69	A5	1206	G
69	A5	1207	G
69	A5	1212	G
69	A5	1213	C
69	A5	1214	G
69	A5	1219	A
69	A5	1220	U
69	A5	1222	A
69	A5	1223	G
69	A5	1226	G
69	A5	1227	C
69	A5	1228	C
69	A5	1229	U
69	A5	1231	A
69	A5	1232	G
69	A5	1233	G
69	A5	1234	G
69	A5	1240	A
69	A5	1241	C
69	A5	1242	G
69	A5	1243	A
69	A5	1245	C
69	A5	1246	U
69	A5	1250	C
69	A5	1253	A
69	A5	1258	C
69	A5	1259	A

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Mol	Chain	Res	Type
69	A5	1260	A
69	A5	1264	U
69	A5	1265	U
69	A5	1270	G
69	A5	1276	G
69	A5	1277	A
69	A5	1279	C
69	A5	1282	U
69	A5	1284	A
69	A5	1285	C
69	A5	1288	U
69	A5	1289	C
69	A5	1290	U
69	A5	1291	U
69	A5	1292	G
69	A5	1293	A
69	A5	1294	U
69	A5	1295	A
69	A5	1296	U
69	A5	1297	G
69	A5	1299	A
69	A5	1303	C
69	A5	1304	A
69	A5	1305	A
69	A5	1307	G
69	A5	1308	U
69	A5	1309	U
69	A5	1310	A
69	A5	1311	U
69	A5	1315	A
69	A5	1316	U
69	A5	1317	A
69	A5	1318	A
69	A5	1321	G
69	A5	1324	C
69	A5	1326	A
69	A5	1330	G
69	A5	1331	G
69	A5	1341	G
69	A5	1342	U
69	A5	1345	G
69	A5	1349	A

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Mol	Chain	Res	Type
69	A5	1350	A
69	A5	1357	C
69	A5	1358	U
69	A5	1359	G
69	A5	1360	U
69	A5	1367	A
69	A5	1368	A
69	A5	1369	C
69	A5	1373	A
69	A5	1374	C
69	A5	1376	U
69	A5	1383	A
69	A5	1384	C
69	A5	1389	C
69	A5	1391	A
69	A5	1393	A
69	A5	1394	U
69	A5	1395	U
69	A5	1396	A
69	A5	1399	A
69	A5	1403	C
69	A5	1404	A
69	A5	1405	U
69	A5	1406	G
69	A5	1407	C
69	A5	1408	A
69	A5	1411	U
69	A5	1416	U
69	A5	1422	G
69	A5	1423	C
69	A5	1424	G
69	A5	1425	U
69	A5	1427	G
69	A5	1435	A
69	A5	1436	A
69	A5	1437	A
69	A5	1438	A
69	A5	1442	C
69	A5	1447	C
69	A5	1448	G
69	A5	1449	G
69	A5	1450	U

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Mol	Chain	Res	Type
69	A5	1451	G
69	A5	1452	A
69	A5	1453	U
69	A5	1455	A
69	A5	1456	U
69	A5	1457	G
69	A5	1458	G
69	A5	1459	A
69	A5	1460	A
69	A5	1461	G
69	A5	1462	U
69	A5	1471	G
69	A5	1472	C
69	A5	1473	U
69	A5	1474	A
69	A5	1475	A
69	A5	1477	G
69	A5	1478	A
69	A5	1479	G
69	A5	1480	U
69	A5	1481	G
69	A5	1482	U
69	A5	1483	G
69	A5	1484	U
69	A5	1485	A
69	A5	1486	A
69	A5	1487	C
69	A5	1488	A
69	A5	1489	A
69	A5	1493	A
69	A5	1498	C
69	A5	1501	A
69	A5	1502	A
69	A5	1505	A
69	A5	1509	A
69	A5	1510	G
69	A5	1520	U
69	A5	1522	G
69	A5	1524	U
69	A5	1531	U
69	A5	1532	A
69	A5	1540	U

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Mol	Chain	Res	Type
69	A5	1546	U
69	A5	1552	A
69	A5	1558	A
69	A5	1564	G
69	A5	1566	U
69	A5	1567	G
69	A5	1568	A
69	A5	1573	U
69	A5	1576	U
69	A5	1578	C
69	A5	1579	U
69	A5	1580	U
69	A5	1581	G
69	A5	1590	A
69	A5	1592	U
69	A5	1593	U
69	A5	1594	U
69	A5	1595	G
69	A5	1596	A
69	A5	1606	G
69	A5	1607	A
69	A5	1619	C
69	A5	1621	A
69	A5	1626	A
69	A5	1627	U
69	A5	1628	G
69	A5	1629	C
69	A5	1632	A
69	A5	1633	G
69	A5	1641	U
69	A5	1643	G
69	A5	1648	A
69	A5	1649	G
69	A5	1658	G
69	A5	1659	A
69	A5	1669	G
69	A5	1671	U
69	A5	1672	A
69	A5	1675	G
69	A5	1678	C
69	A5	1687	U
69	A5	1688	A

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Mol	Chain	Res	Type
69	A5	1689	G
69	A5	1690	U
69	A5	1692	G
69	A5	1697	U
69	A5	1698	A
69	A5	1699	A
69	A5	1712	C
69	A5	1713	U
69	A5	1714	U
69	A5	1723	G
69	A5	1724	A
69	A5	1727	U
69	A5	1728	G
69	A5	1730	A
69	A5	1731	G
69	A5	1736	G
69	A5	1745	G
69	A5	1746	A
69	A5	1750	G
69	A5	1751	U
69	A5	1754	U
69	A5	1755	U
69	A5	1763	A
69	A5	1765	U
69	A5	1766	U
69	A5	1769	U
69	A5	1774	C
69	A5	1776	U
69	A5	1778	A
69	A5	1779	G
69	A5	1782	C
69	A5	1784	A
69	A5	1785	G
69	A5	1786	G
69	A5	1792	G
69	A5	1793	C
69	A5	1794	G
69	A5	1795	A
69	A5	1796	A
69	A5	1797	A
69	A5	1798	A
69	A5	1799	U

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Mol	Chain	Res	Type
69	A5	1800	U
69	A5	1801	U
69	A5	1802	U
69	A5	1803	C
69	A5	1804	A
69	A5	1807	U
69	A5	1808	A
69	A5	1809	A
69	A5	1811	A
69	A5	1812	C
69	A5	1813	A
69	A5	1860	A
69	A5	1861	A
69	A5	1863	U
69	A5	1864	U
69	A5	1865	U
69	A5	1866	G
69	A5	1867	A
69	A5	1871	A
69	A5	1872	A
69	A5	1873	A
69	A5	1874	G
69	A5	1877	A
69	A5	1885	U
69	A5	1889	A
69	A5	1890	U
69	A5	1892	C
69	A5	1908	A
69	A5	1910	C
69	A5	1911	C
69	A5	1913	U
69	A5	1914	U
69	A5	1918	U
69	A5	1923	A
69	A5	1924	A
69	A5	1925	U
69	A5	1926	A
69	A5	1927	U
69	A5	1931	C
69	A5	1934	C
69	A5	1935	G
69	A5	1937	G

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Mol	Chain	Res	Type
69	A5	1944	C
69	A5	1948	C
69	A5	1951	C
69	A5	1952	A
69	A5	1954	G
69	A5	1956	A
69	A5	1957	C
69	A5	1958	G
69	A5	1959	A
69	A5	1960	C
69	A5	1961	C
69	A5	1970	G
69	A5	1973	G
69	A5	1986	G
69	A5	1997	C
69	A5	1998	U
69	A5	2004	G
69	A5	2005	U
69	A5	2013	C
69	A5	2014	C
69	A5	2015	G
69	A5	2016	U
69	A5	2017	A
69	A5	2030	U
69	A5	2035	C
69	A5	2037	C
69	A5	2038	A
69	A5	2052	G
69	A5	2053	A
69	A5	2054	U
69	A5	2055	G
69	A5	2057	G
69	A5	2061	G
69	A5	2062	A
69	A5	2063	A
69	A5	2064	G
69	A5	2065	A
69	A5	2066	G
69	A5	2070	G
69	A5	2075	A
69	A5	2076	U
69	A5	2077	A

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Mol	Chain	Res	Type
69	A5	2078	C
69	A5	2079	U
69	A5	2082	U
69	A5	2084	U
69	A5	2088	G
69	A5	2091	A
69	A5	2092	U
69	A5	2093	U
69	A5	2094	U
69	A5	2103	G
69	A5	2104	A
69	A5	2105	C
69	A5	2106	C
69	A5	2110	A
69	A5	2112	A
69	A5	2122	G
69	A5	2125	G
69	A5	2126	A
69	A5	2127	C
69	A5	2128	A
69	A5	2129	C
69	A5	2130	G
69	A5	2131	C
69	A5	2132	A
69	A5	2133	A
69	A5	2134	A
69	A5	2135	C
69	A5	2136	U
69	A5	2137	U
69	A5	2140	C
69	A5	2148	C
69	A5	2151	A
69	A5	2155	A
69	A5	2156	U
69	A5	2157	A
69	A5	2158	U
69	A5	2166	U
69	A5	2167	G
69	A5	2170	C
69	A5	2171	U
69	A5	2174	A
69	A5	2183	A

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Mol	Chain	Res	Type
69	A5	2194	G
69	A5	2195	A
69	A5	2196	U
69	A5	2202	A
69	A5	2205	G
69	A5	2206	U
69	A5	2212	A
69	A5	2216	A
69	A5	2222	G
69	A5	2224	A
69	A5	2230	G
69	A5	2239	C
69	A5	2241	U
69	A5	2242	C
69	A5	2247	U
69	A5	2258	U
69	A5	2259	C
69	A5	2267	U
69	A5	2268	G
69	A5	2269	A
69	A5	2270	G
69	A5	2272	U
69	A5	2273	A
69	A5	2274	G
69	A5	2277	G
69	A5	2462	U
69	A5	2464	A
69	A5	2467	A
69	A5	2469	U
69	A5	2470	U
69	A5	2471	A
69	A5	2472	A
69	A5	2475	A
69	A5	2479	A
69	A5	2480	U
69	A5	2483	A
69	A5	2490	G
69	A5	2491	C
69	A5	2493	C
69	A5	2499	U
69	A5	2500	G
69	A5	2501	G

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Mol	Chain	Res	Type
69	A5	2505	A
69	A5	2510	A
69	A5	2513	G
69	A5	2519	U
69	A5	2523	A
69	A5	2525	C
69	A5	2528	A
69	A5	2529	G
69	A5	2534	G
69	A5	2537	A
69	A5	2538	U
69	A5	2545	A
69	A5	2546	G
69	A5	2547	C
69	A5	2548	G
69	A5	2549	G
69	A5	2554	U
69	A5	2555	G
69	A5	2557	C
69	A5	2562	U
69	A5	2565	G
69	A5	2566	A
69	A5	2570	C
69	A5	2572	G
69	A5	2575	C
69	A5	2583	U
69	A5	2584	G
69	A5	2585	A
69	A5	2586	A
69	A5	2587	U
69	A5	2588	G
69	A5	2601	A
69	A5	2603	U
69	A5	2609	U
69	A5	2610	A
69	A5	2622	A
69	A5	2626	C
69	A5	2627	G
69	A5	2633	A
69	A5	2634	A
69	A5	2635	C
69	A5	2640	A

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Mol	Chain	Res	Type
69	A5	2641	C
69	A5	2643	C
69	A5	2646	U
69	A5	2650	G
69	A5	2651	G
69	A5	2654	G
69	A5	2659	A
69	A5	2660	U
69	A5	2663	C
69	A5	2665	C
69	A5	2666	G
69	A5	2676	U
69	A5	2681	A
69	A5	2683	G
69	A5	2684	C
69	A5	2685	G
69	A5	2686	C
69	A5	2688	U
69	A5	2691	A
69	A5	2693	G
69	A5	2701	G
69	A5	2708	C
69	A5	2713	G
69	A5	2714	U
69	A5	2725	U
69	A5	2727	U
69	A5	2733	G
69	A5	2741	A
69	A5	2743	C
69	A5	2744	C
69	A5	2745	A
69	A5	2750	A
69	A5	2751	A
69	A5	2752	C
69	A5	2753	G
69	A5	2754	G
69	A5	2760	G
69	A5	2768	A
69	A5	2771	G
69	A5	2775	A
69	A5	2779	A
69	A5	2780	A

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Mol	Chain	Res	Type
69	A5	2781	G
69	A5	2789	U
69	A5	2792	G
69	A5	2796	G
69	A5	2797	A
69	A5	2803	A
69	A5	2813	G
69	A5	2815	A
69	A5	2816	A
69	A5	2817	G
69	A5	2819	A
69	A5	2821	A
69	A5	2822	C
69	A5	2825	A
69	A5	2826	A
69	A5	2828	A
69	A5	2831	U
69	A5	2832	G
69	A5	2834	A
69	A5	2836	A
69	A5	2837	A
69	A5	2839	A
69	A5	2840	A
69	A5	2842	U
69	A5	2844	G
69	A5	2845	G
69	A5	2847	G
69	A5	2848	A
69	A5	2869	U
69	A5	2870	C
69	A5	2871	G
69	A5	2873	C
69	A5	2876	U
69	A5	2877	G
69	A5	2880	A
69	A5	2881	U
69	A5	2882	A
69	A5	2883	C
69	A5	2884	C
69	A5	2886	C
69	A5	2887	U
69	A5	2888	A

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Mol	Chain	Res	Type
69	A5	2891	C
69	A5	2893	U
69	A5	2895	U
69	A5	2896	U
69	A5	2898	U
69	A5	2899	U
69	A5	2900	U
69	A5	2901	C
69	A5	2902	C
69	A5	2908	U
69	A5	2916	U
69	A5	2917	A
69	A5	2918	A
69	A5	2922	G
69	A5	2923	A
69	A5	2925	C
69	A5	2931	U
69	A5	2932	C
69	A5	2989	G
69	A5	2990	C
69	A5	2991	A
69	A5	2992	A
69	A5	2994	C
69	A5	2995	U
69	A5	2997	C
69	A5	2998	U
69	A5	3000	G
69	A5	3003	C
69	A5	3004	A
69	A5	3005	A
69	A5	3008	U
69	A5	3011	C
69	A5	3014	G
69	A5	3015	A
69	A5	3016	G
69	A5	3103	U
69	A5	3104	C
69	A5	3105	A
69	A5	3116	A
69	A5	3117	A
69	A5	3118	U
69	A5	3119	U

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Mol	Chain	Res	Type
69	A5	3123	G
69	A5	3125	A
69	A5	3126	C
69	A5	3128	U
69	A5	3129	U
69	A5	3132	C
69	A5	3138	G
69	A5	3139	G
69	A5	3140	G
69	A5	3146	G
69	A5	3147	A
69	A5	3158	A
69	A5	3169	A
69	A5	3170	U
69	A5	3173	U
69	A5	3174	A
69	A5	3183	G
69	A5	3184	U
69	A5	3185	C
69	A5	3188	A
69	A5	3189	A
69	A5	3190	G
69	A5	3191	G
69	A5	3204	G
69	A5	3209	G
69	A5	3211	A
69	A5	3212	A
69	A5	3213	C
69	A5	3219	A
69	A5	3220	U
69	A5	3221	A
69	A5	3223	A
69	A5	3227	A
69	A5	3228	A
69	A5	3229	A
69	A5	3233	C
69	A5	3235	A
69	A5	3236	A
69	A5	3241	G
69	A5	3244	U
69	A5	3245	U
69	A5	3246	G

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Mol	Chain	Res	Type
69	A5	3247	A
69	A5	3248	U
69	A5	3252	G
69	A5	3258	C
69	A5	3259	A
69	A5	3260	G
69	A5	3261	U
69	A5	3266	A
69	A5	3270	G
69	A5	3272	A
69	A5	3278	A
69	A5	3280	A
69	A5	3281	G
69	A5	3282	C
69	A5	3283	U
69	A5	3284	C
69	A5	3285	G
69	A5	3287	C
69	A5	3294	A
69	A5	3298	U
69	A5	3299	U
69	A5	3300	U
69	A5	3303	G
69	A5	3304	U
69	A5	3305	U
69	A5	3306	U
69	A5	3308	A
69	A5	3309	A
69	A5	3311	A
69	A5	3319	A
69	A5	3321	A
69	A5	3324	A
69	A5	3326	G
69	A5	3328	G
69	A5	3329	U
69	A5	3331	A
69	A5	3332	G
69	A5	3333	A
69	A5	3334	A
69	A5	3337	G
69	A5	3341	C
69	A5	3342	C

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Mol	Chain	Res	Type
69	A5	3345	A
69	A5	3346	G
69	A5	3348	G
69	A5	3349	A
69	A5	3350	U
69	A5	3359	U
69	A5	3360	G
69	A5	3361	U
69	A5	3373	G
69	A5	3374	U
69	A5	3375	U
69	A5	3377	A
69	A5	3378	U
69	A5	3379	A
69	A5	3381	C
69	A5	3392	U
69	A5	3395	G
69	A5	3397	U
69	A5	3399	C
69	A5	3401	U
69	A5	3403	G
69	A5	3404	A
69	A5	3405	U
69	A5	3408	C
69	A5	3418	U
69	A5	3419	A
69	A5	3426	U
69	A5	3430	G
69	A5	3431	C
69	A5	3436	U
69	A5	3443	A
69	A5	3448	U
69	A5	3455	U
69	A5	3456	U
69	A5	3457	C
69	A5	3465	C
69	A5	3466	A
69	A5	3467	A
69	A5	3468	G
69	A5	3470	G
69	A5	3473	C
69	A5	3478	G

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Mol	Chain	Res	Type
69	A5	3482	G
69	A5	3486	U
69	A5	3487	A
69	A5	3488	G
69	A5	3490	C
69	A5	3496	U
69	A5	3499	G
69	A5	3502	A
69	A5	3509	U
69	A5	3510	U
69	A5	3511	U
69	A5	3514	C
69	A5	3515	C
69	A5	3516	C
69	A5	3518	A
69	A5	3520	U
69	A5	3521	A
69	A5	3523	U
69	A5	3527	A
69	A5	3529	A
69	A5	3530	A
69	A5	3531	C
69	A5	3532	G
69	A5	3535	G
69	A5	3540	G
69	A5	3541	A
69	A5	3546	A
69	A5	3547	U
69	A5	3549	C
69	A5	3556	A
69	A5	3558	U
69	A5	3563	G
69	A5	3568	A
69	A5	3569	C
69	A5	3581	G
69	A5	3584	C
69	A5	3585	A
69	A5	3591	A
69	A5	3592	C
69	A5	3593	A
69	A5	3594	A
69	A5	3599	U

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Mol	Chain	Res	Type
69	A5	3604	G
69	A5	3608	G
69	A5	3609	A
69	A5	3613	G
69	A5	3614	U
69	A5	3621	A
69	A5	3626	A
69	A5	3627	C
69	A5	3628	G
69	A5	3629	U
69	A5	3633	U
69	A5	3635	G
69	A5	3638	U
69	A5	3649	C
69	A5	3650	G
69	A5	3654	C
69	A5	3656	A
69	A5	3661	C
69	A5	3664	A
69	A5	3665	U
69	A5	3671	C
69	A5	3672	U
69	A5	3675	A
69	A5	3676	C
69	A5	3677	U
69	A5	3678	G
69	A5	3684	A
69	A5	3685	U
69	A5	3686	A
69	A5	3687	A
69	A5	3688	A
69	A5	3689	U
69	A5	3690	A
69	A5	3694	G
69	A5	3695	G
69	A5	3696	C
69	A5	3697	A
69	A5	3698	A
69	A5	3699	U
69	A5	3700	U
69	A5	3701	U
69	A5	3702	G

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Mol	Chain	Res	Type
69	A5	3705	U
69	A5	3708	U
69	A5	3711	G
69	A5	3712	G
69	A5	3713	C
69	A5	3715	U
69	A5	3718	A
69	A5	3719	A
69	A5	3720	A
69	A5	3721	C
69	A5	3722	C
69	A5	3723	A
69	A5	3725	U
69	A5	3726	U
69	A5	3727	A
69	A5	3728	A
69	A5	3729	A
69	A5	3730	G
69	A5	3731	U
69	A5	3732	U
69	A5	3738	U
69	A5	3739	U
69	A5	3742	C
69	A5	3751	C
69	A5	3752	G
69	A5	3753	A
69	A5	3754	C
69	A5	3755	A
69	A5	3756	A
69	A5	3757	U
69	A5	3758	G
69	A5	3759	G
69	A5	3761	U
69	A5	3762	G
69	A5	3763	U
69	A5	3764	G
69	A5	3765	A
69	A5	3766	U
69	A5	3767	G
69	A5	3769	C
69	A5	3772	U
69	A5	3773	G

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Mol	Chain	Res	Type
69	A5	3774	U
69	A5	3775	A
69	A5	3776	A
69	A5	3777	U
69	A5	3778	U
69	A5	3779	U
69	A5	3782	A
69	A5	3783	A
69	A5	3784	C
69	A5	3785	A
69	A5	3788	G
69	A5	3791	A
69	A5	3792	A
69	A5	3794	U
69	A5	3795	G
69	A5	3796	G
69	A5	3798	A
69	A5	3802	U
69	A5	3803	C
69	A5	3804	U
69	A5	3805	U
69	A5	3807	G
69	A5	3808	A
69	A5	3809	U
69	A5	3810	C
69	A5	3811	A
69	A5	3812	C
69	A5	3814	U
69	A5	3815	G
69	A5	3816	A
69	A5	3818	G
69	A5	3820	C
69	A5	3821	G
69	A5	3825	U
69	A5	3828	U
69	A5	3830	A
69	A5	3832	A
69	A5	3837	A
69	A5	3839	A
69	A5	3840	G
69	A5	3841	C
69	A5	3842	A

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Mol	Chain	Res	Type
69	A5	3843	U
69	A5	3844	U
69	A5	3845	A
69	A5	3846	U
69	A5	3847	U
69	A5	3848	U
69	A5	3851	U
69	A5	3854	A
69	A5	3856	U
69	A5	3860	A
69	A5	3861	A
69	A5	3862	A
69	A5	3865	C
69	A5	3867	A
69	A5	3868	G
69	A5	3869	A
69	A5	3877	G
69	A5	3878	U
69	A5	3881	A
69	A5	3887	U
69	A5	3888	U
69	A5	3891	U
69	A5	3892	A
69	A5	3894	C
69	A5	3895	A
69	A5	3896	G
69	A5	3898	C
69	A5	3903	U
69	A5	3908	U
69	A5	3915	U
69	A5	3916	U
69	A5	3919	G
69	A5	3921	A
69	A5	3922	G
69	A5	3925	G
69	A5	3926	C
69	A5	3927	C
69	A5	3929	U
69	A5	3930	A
69	A5	3932	U
69	A5	3933	G
69	A5	3935	G

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Mol	Chain	Res	Type
69	A5	3937	U
69	A5	3942	U
69	A5	3943	G
69	A5	3949	U
69	A5	3952	C
69	A5	3955	U
69	A5	3956	U
69	A5	3957	G
69	A5	3962	A
69	A5	3963	U
69	A5	3964	G
69	A5	3967	U
69	A5	3970	A
70	B2	2	U
70	B2	3	U
70	B2	5	U
70	B2	20	G
70	B2	25	U
70	B2	26	A
70	B2	35	U
70	B2	38	C
70	B2	42	G
70	B2	47	A
70	B2	48	G
70	B2	49	C
70	B2	57	G
70	B2	60	U
70	B2	63	G
70	B2	65	A
70	B2	66	C
70	B2	67	A
70	B2	68	C
70	B2	70	C
70	B2	71	G
70	B2	72	A
70	B2	74	U
70	B2	76	A
70	B2	77	A
70	B2	78	A
70	B2	79	A
70	B2	80	G
70	B2	82	G

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Mol	Chain	Res	Type
70	B2	92	A
70	B2	99	A
70	B2	103	U
70	B2	105	U
70	B2	113	G
70	B2	114	G
70	B2	115	U
70	B2	121	A
70	B2	126	G
70	B2	127	U
70	B2	136	A
70	B2	137	C
70	B2	138	U
70	B2	141	G
70	B2	142	A
70	B2	143	U
70	B2	150	G
70	B2	153	A
70	B2	155	U
70	B2	156	U
70	B2	157	C
70	B2	158	U
70	B2	163	C
70	B2	166	A
70	B2	173	C
70	B2	174	A
70	B2	175	A
70	B2	177	U
70	B2	178	A
70	B2	183	A
70	B2	185	G
70	B2	187	A
70	B2	188	C
70	B2	189	C
70	B2	190	U
70	B2	191	U
70	B2	193	U
70	B2	194	G
70	B2	195	G
70	B2	196	G
70	B2	200	U
70	B2	203	G

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Mol	Chain	Res	Type
70	B2	204	C
70	B2	214	G
70	B2	215	C
70	B2	216	U
70	B2	217	A
70	B2	218	A
70	B2	225	G
70	B2	235	G
70	B2	238	C
70	B2	243	U
70	B2	248	G
70	B2	249	U
70	B2	250	U
70	B2	251	G
70	B2	252	A
70	B2	253	A
70	B2	256	C
70	B2	257	U
70	B2	258	A
70	B2	265	A
70	B2	266	U
70	B2	267	G
70	B2	270	G
70	B2	271	A
70	B2	276	A
70	B2	277	U
70	B2	279	G
70	B2	280	U
70	B2	281	C
70	B2	282	U
70	B2	283	U
70	B2	284	G
70	B2	285	U
70	B2	286	A
70	B2	287	C
70	B2	288	C
70	B2	289	G
70	B2	292	G
70	B2	293	A
70	B2	295	A
70	B2	301	U
70	B2	303	C

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Mol	Chain	Res	Type
70	B2	304	A
70	B2	306	A
70	B2	311	U
70	B2	312	G
70	B2	319	C
70	B2	321	A
70	B2	326	U
70	B2	327	G
70	B2	329	U
70	B2	334	G
70	B2	342	G
70	B2	343	A
70	B2	348	C
70	B2	355	G
70	B2	357	A
70	B2	364	A
70	B2	366	C
70	B2	379	U
70	B2	382	G
70	B2	392	A
70	B2	395	G
70	B2	405	A
70	B2	407	C
70	B2	409	G
70	B2	417	A
70	B2	421	A
70	B2	422	A
70	B2	423	G
70	B2	424	G
70	B2	428	G
70	B2	429	C
70	B2	430	A
70	B2	431	G
70	B2	439	G
70	B2	440	U
70	B2	444	U
70	B2	448	C
70	B2	449	C
70	B2	453	C
70	B2	458	C
70	B2	459	U
70	B2	464	G

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Mol	Chain	Res	Type
70	B2	466	G
70	B2	469	A
70	B2	480	A
70	B2	481	U
70	B2	482	A
70	B2	485	A
70	B2	489	C
70	B2	499	A
70	B2	501	C
70	B2	502	C
70	B2	506	G
70	B2	508	C
70	B2	509	C
70	B2	510	U
70	B2	512	U
70	B2	513	A
70	B2	514	A
70	B2	515	U
70	B2	516	U
70	B2	520	A
70	B2	521	U
70	B2	522	G
70	B2	523	A
70	B2	527	C
70	B2	535	A
70	B2	541	U
70	B2	546	A
70	B2	547	G
70	B2	548	G
70	B2	549	A
70	B2	550	C
70	B2	551	C
70	B2	552	A
70	B2	556	G
70	B2	559	G
70	B2	562	C
70	B2	564	A
70	B2	565	G
70	B2	566	U
70	B2	567	C
70	B2	573	C
70	B2	576	G

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Mol	Chain	Res	Type
70	B2	583	C
70	B2	586	U
70	B2	587	A
70	B2	588	A
70	B2	591	C
70	B2	595	C
70	B2	596	U
70	B2	599	A
70	B2	602	A
70	B2	603	G
70	B2	614	A
70	B2	615	G
70	B2	617	U
70	B2	619	U
70	B2	621	G
70	B2	627	A
70	B2	628	A
70	B2	629	A
70	B2	630	A
70	B2	631	C
70	B2	632	G
70	B2	641	U
70	B2	646	U
70	B2	647	U
70	B2	649	U
70	B2	653	U
70	B2	655	A
70	B2	656	U
70	B2	657	A
70	B2	658	C
70	B2	705	G
70	B2	712	U
70	B2	713	A
70	B2	714	U
70	B2	715	U
70	B2	720	G
70	B2	820	G
70	B2	824	U
70	B2	825	A
70	B2	833	G
70	B2	837	A
70	B2	843	G

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Mol	Chain	Res	Type
70	B2	847	G
70	B2	848	C
70	B2	852	A
70	B2	856	A
70	B2	857	G
70	B2	861	U
70	B2	862	C
70	B2	863	A
70	B2	865	A
70	B2	866	U
70	B2	873	A
70	B2	874	U
70	B2	877	U
70	B2	878	C
70	B2	879	U
70	B2	880	G
70	B2	882	G
70	B2	895	A
70	B2	898	U
70	B2	899	A
70	B2	900	A
70	B2	901	G
70	B2	903	C
70	B2	904	C
70	B2	905	U
70	B2	906	C
70	B2	907	U
70	B2	908	G
70	B2	909	U
70	B2	911	C
70	B2	913	G
70	B2	916	U
70	B2	918	C
70	B2	925	U
70	B2	929	A
70	B2	930	G
70	B2	932	U
70	B2	935	A
70	B2	936	G
70	B2	937	A
70	B2	938	G
70	B2	939	G

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Mol	Chain	Res	Type
70	B2	940	U
70	B2	941	A
70	B2	942	A
70	B2	943	U
70	B2	947	U
70	B2	948	A
70	B2	949	A
70	B2	950	U
70	B2	957	A
70	B2	958	G
70	B2	960	U
70	B2	963	G
70	B2	973	U
70	B2	978	C
70	B2	989	G
70	B2	993	A
70	B2	999	U
70	B2	1000	G
70	B2	1001	G
70	B2	1007	C
70	B2	1008	G
70	B2	1013	A
70	B2	1019	U
70	B2	1020	U
70	B2	1021	A
70	B2	1022	A
70	B2	1026	A
70	B2	1031	A
70	B2	1032	U
70	B2	1033	U
70	B2	1042	A
70	B2	1047	U
70	B2	1053	A
70	B2	1060	A
70	B2	1070	A
70	B2	1075	U
70	B2	1079	A
70	B2	1080	A
70	B2	1090	A
70	B2	1091	U
70	B2	1092	A
70	B2	1096	C

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Mol	Chain	Res	Type
70	B2	1098	C
70	B2	1110	A
70	B2	1112	A
70	B2	1113	A
70	B2	1115	C
70	B2	1116	G
70	B2	1126	A
70	B2	1127	G
70	B2	1137	G
70	B2	1138	U
70	B2	1139	A
70	B2	1140	G
70	B2	1141	C
70	B2	1145	U
70	B2	1159	C
70	B2	1161	G
70	B2	1167	U
70	B2	1168	C
70	B2	1170	G
70	B2	1178	A
70	B2	1179	A
70	B2	1183	U
70	B2	1184	U
70	B2	1185	U
70	B2	1186	U
70	B2	1187	U
70	B2	1188	G
70	B2	1201	A
70	B2	1217	U
70	B2	1226	A
70	B2	1234	G
70	B2	1236	C
70	B2	1238	G
70	B2	1239	A
70	B2	1240	A
70	B2	1243	G
70	B2	1245	A
70	B2	1246	C
70	B2	1247	C
70	B2	1248	A
70	B2	1261	C
70	B2	1262	C

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Mol	Chain	Res	Type
70	B2	1273	U
70	B2	1274	U
70	B2	1275	U
70	B2	1278	C
70	B2	1281	A
70	B2	1282	A
70	B2	1284	A
70	B2	1285	C
70	B2	1287	G
70	B2	1288	G
70	B2	1290	A
70	B2	1300	G
70	B2	1302	U
70	B2	1304	G
70	B2	1305	A
70	B2	1307	C
70	B2	1308	A
70	B2	1309	U
70	B2	1311	A
70	B2	1313	U
70	B2	1314	G
70	B2	1315	U
70	B2	1316	G
70	B2	1319	A
70	B2	1321	A
70	B2	1322	C
70	B2	1323	A
70	B2	1327	U
70	B2	1328	G
70	B2	1329	A
70	B2	1330	U
70	B2	1331	A
70	B2	1332	G
70	B2	1333	C
70	B2	1338	U
70	B2	1339	C
70	B2	1343	A
70	B2	1344	A
70	B2	1345	U
70	B2	1346	C
70	B2	1347	U
70	B2	1348	A

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Mol	Chain	Res	Type
70	B2	1349	U
70	B2	1351	G
70	B2	1352	G
70	B2	1353	U
70	B2	1354	G
70	B2	1356	U
70	B2	1360	G
70	B2	1371	C
70	B2	1372	U
70	B2	1373	U
70	B2	1378	C
70	B2	1381	G
70	B2	1382	G
70	B2	1383	A
70	B2	1384	G
70	B2	1386	G
70	B2	1387	A
70	B2	1388	U
70	B2	1390	U
70	B2	1391	G
70	B2	1392	U
70	B2	1393	C
70	B2	1394	U
70	B2	1395	G
70	B2	1396	G
70	B2	1397	U
70	B2	1399	A
70	B2	1400	A
70	B2	1401	U
70	B2	1402	U
70	B2	1404	C
70	B2	1405	G
70	B2	1407	U
70	B2	1408	A
70	B2	1409	A
70	B2	1410	C
70	B2	1412	A
70	B2	1427	U
70	B2	1428	A
70	B2	1432	A
70	B2	1433	A
70	B2	1434	U

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Mol	Chain	Res	Type
70	B2	1436	G
70	B2	1443	U
70	B2	1444	C
70	B2	1445	A
70	B2	1446	G
70	B2	1447	G
70	B2	1448	A
70	B2	1449	U
70	B2	1450	U
70	B2	1453	G
70	B2	1455	U
70	B2	1457	C
70	B2	1458	U
70	B2	1459	G
70	B2	1460	A
70	B2	1467	U
70	B2	1469	U
70	B2	1470	A
70	B2	1520	A
70	B2	1521	U
70	B2	1524	A
70	B2	1529	G
70	B2	1530	A
70	B2	1531	G
70	B2	1534	G
70	B2	1538	C
70	B2	1542	U
70	B2	1543	G
70	B2	1546	U
70	B2	1547	U
70	B2	1548	G
70	B2	1549	U
70	B2	1551	C
70	B2	1560	G
70	B2	1565	C
70	B2	1566	U
70	B2	1572	C
70	B2	1574	U
70	B2	1575	A
70	B2	1576	A
70	B2	1578	U
70	B2	1581	A

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Mol	Chain	Res	Type
70	B2	1583	A
70	B2	1584	A
70	B2	1588	G
70	B2	1589	C
70	B2	1590	G
70	B2	1591	U
70	B2	1592	C
70	B2	1593	U
70	B2	1594	A
70	B2	1596	C
70	B2	1597	A
70	B2	1599	U
70	B2	1600	A
70	B2	1601	A
70	B2	1602	U
70	B2	1603	G
70	B2	1605	G
70	B2	1606	A
70	B2	1607	U
70	B2	1610	A
70	B2	1613	A
70	B2	1619	A
70	B2	1620	G
70	B2	1623	C
70	B2	1624	U
70	B2	1625	G
70	B2	1627	G
70	B2	1628	A
70	B2	1636	A
70	B2	1638	A
70	B2	1639	U
70	B2	1642	C
70	B2	1643	C
70	B2	1644	U
70	B2	1651	C
70	B2	1652	A
70	B2	1661	A
70	B2	1663	A
70	B2	1665	U
70	B2	1666	G
70	B2	1674	C
70	B2	1675	A

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Mol	Chain	Res	Type
70	B2	1680	G
70	B2	1682	A
70	B2	1684	U
70	B2	1685	U
70	B2	1686	C
70	B2	1688	U
70	B2	1698	G
70	B2	1709	A
70	B2	1710	C
70	B2	1712	G
70	B2	1714	U
70	B2	1715	G
70	B2	1716	A
70	B2	1717	A
70	B2	1718	C
70	B2	1719	C
70	B2	1727	U
70	B2	1729	C
70	B2	1732	G
70	B2	1737	U
70	B2	1741	A
70	B2	1742	A
70	B2	1749	C
70	B2	1751	G
70	B2	1752	U
70	B2	1755	A
70	B2	1757	G
70	B2	1758	A
70	B2	1760	G
70	B2	1765	U
70	B2	1766	G
70	B2	1775	A
70	B2	1782	G
70	B2	1788	C
70	B2	1793	A
70	B2	1797	G
70	B2	1808	G
70	B2	1811	C
70	B2	1814	G
70	B2	1816	C
70	B2	1821	G
70	B2	1822	U

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Mol	Chain	Res	Type
70	B2	1823	A
70	B2	1826	C
70	B2	1827	A
70	B2	1828	C
70	B2	1830	G
70	B2	1831	C
70	B2	1835	U
70	B2	1840	A
70	B2	1849	U
70	B2	1850	G
70	B2	1855	A
70	B2	1857	U
70	B2	1861	U
70	B2	1870	C
70	B2	1872	G
70	B2	1874	C
70	B2	1875	G
70	B2	1876	U
70	B2	1881	A
70	B2	1882	C
70	B2	1898	G
70	B2	1903	G
70	B2	1905	U
70	B2	1906	U
70	B2	1912	G
70	B2	1914	A
70	B2	1925	G
70	B2	1926	A
70	B2	1934	U
70	B2	1936	U
70	B2	1942	G
70	B2	1949	A
70	B2	1950	A
70	B2	1951	A
70	B2	1952	G
70	B2	1956	U
70	B2	1960	A
70	B2	1961	A
70	B2	1962	G
70	B2	1963	G
70	B2	1964	U
70	B2	1971	A

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Mol	Chain	Res	Type
70	B2	1975	G
70	B2	1977	A
70	B2	1987	G
70	B2	1988	G
70	B2	1989	A
70	B2	1990	U
70	B2	1991	C
70	B2	1993	U
70	B2	1994	U
70	B2	1995	A

All (116) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
38	A9	21	G
39	A7	119	C
40	A8	108	A
69	A5	29	U
69	A5	47	A
69	A5	89	A
69	A5	123	U
69	A5	190	A
69	A5	296	C
69	A5	419	U
69	A5	440	U
69	A5	523	C
69	A5	580	A
69	A5	615	C
69	A5	621	A
69	A5	640	U
69	A5	652	G
69	A5	662	A
69	A5	670	G
69	A5	750	G
69	A5	751	A
69	A5	774	A
69	A5	775	U
69	A5	839	A
69	A5	840	U
69	A5	871	A
69	A5	872	A
69	A5	926	U

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Mol	Chain	Res	Type
69	A5	1096	A
69	A5	1116	G
69	A5	1159	C
69	A5	1197	A
69	A5	1206	G
69	A5	1290	U
69	A5	1293	A
69	A5	1294	U
69	A5	1308	U
69	A5	1310	A
69	A5	1324	C
69	A5	1407	C
69	A5	1565	A
69	A5	1566	U
69	A5	1594	U
69	A5	1659	A
69	A5	1688	A
69	A5	1689	G
69	A5	1713	U
69	A5	1784	A
69	A5	1785	G
69	A5	1798	A
69	A5	1799	U
69	A5	1801	U
69	A5	1862	U
69	A5	1889	A
69	A5	1909	U
69	A5	2062	A
69	A5	2093	U
69	A5	2125	G
69	A5	2129	C
69	A5	2155	A
69	A5	2174	A
69	A5	2491	C
69	A5	2750	A
69	A5	2796	G
69	A5	2868	A
69	A5	2993	G
69	A5	3118	U
69	A5	3247	A
69	A5	3350	U
69	A5	3359	U

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Mol	Chain	Res	Type
69	A5	3591	A
69	A5	3608	G
69	A5	3627	C
69	A5	3711	G
69	A5	3728	A
69	A5	3729	A
69	A5	3730	G
69	A5	3754	C
69	A5	3757	U
69	A5	3760	A
69	A5	3761	U
69	A5	3839	A
69	A5	3861	A
69	A5	3969	G
70	B2	25	U
70	B2	113	G
70	B2	172	G
70	B2	256	C
70	B2	278	G
70	B2	378	G
70	B2	381	C
70	B2	422	A
70	B2	488	A
70	B2	511	G
70	B2	566	U
70	B2	704	U
70	B2	878	C
70	B2	937	A
70	B2	1138	U
70	B2	1185	U
70	B2	1186	U
70	B2	1196	G
70	B2	1245	A
70	B2	1284	A
70	B2	1329	A
70	B2	1331	A
70	B2	1400	A
70	B2	1519	U
70	B2	1546	U
70	B2	1595	G
70	B2	1673	U
70	B2	1748	A

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Mol	Chain	Res	Type
70	B2	1765	U
70	B2	1807	C
70	B2	1949	A
70	B2	1992	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
69	A5	7
70	B2	5
72	AT	1
7	CI	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AT	107:LEU	C	121:ARG	N	19.55
1	A5	2293:C	O3'	2390:U	P	18.82
1	A5	2941:G	O3'	2976:A	P	18.19
1	B2	738:A	O3'	757:U	P	14.79
1	A5	2406:A	O3'	2452:A	P	13.09

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A5	3039:A	O3'	3083:U	P	11.82
1	B2	1236:C	O3'	1237:G	P	9.97
1	B2	1479:U	O3'	1501:A	P	6.62
1	A5	1177:U	O3'	1182:A	P	6.09
1	A5	2896:U	O3'	2897:G	P	5.83
1	A5	2819:A	O3'	2820:G	P	5.66
1	B2	666:A	O3'	687:U	P	5.55
1	B2	1817:C	O3'	1818:U	P	3.74
1	CI	132:GLY	C	133:GLN	N	1.18

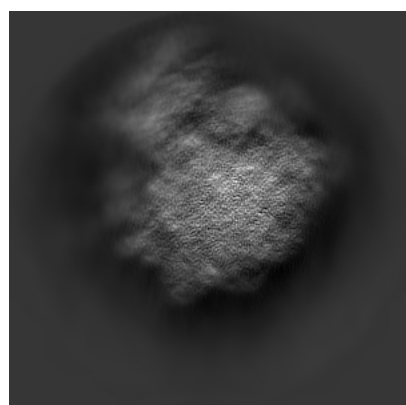
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10624. These allow visual inspection of the internal detail of the map and identification of artifacts.

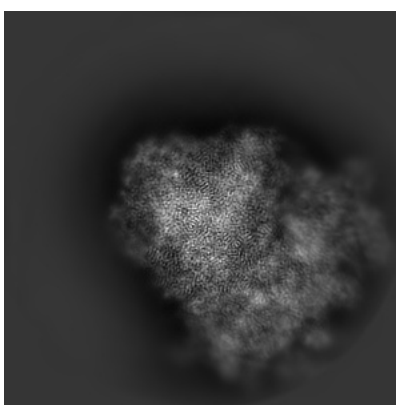
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

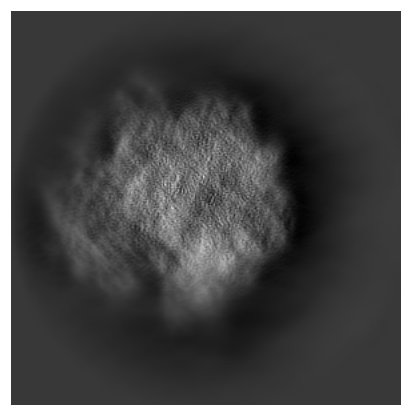
6.1.1 Primary map



X



Y

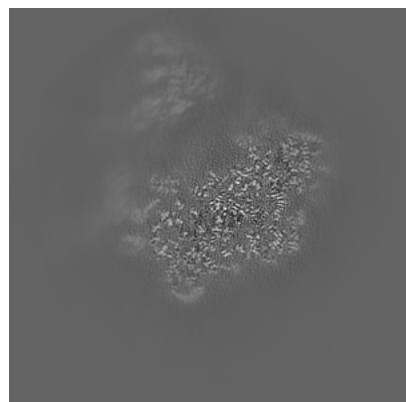


Z

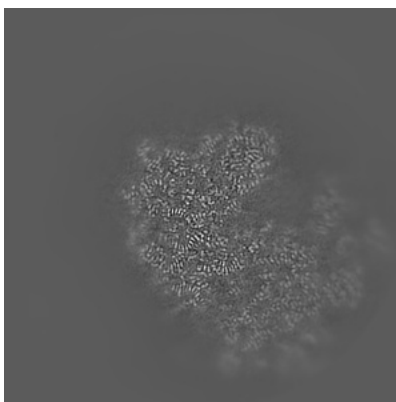
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

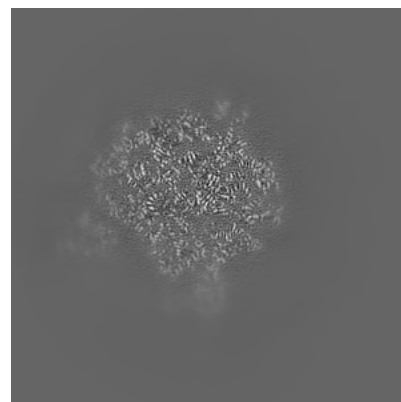
6.2.1 Primary map



X Index: 200



Y Index: 200

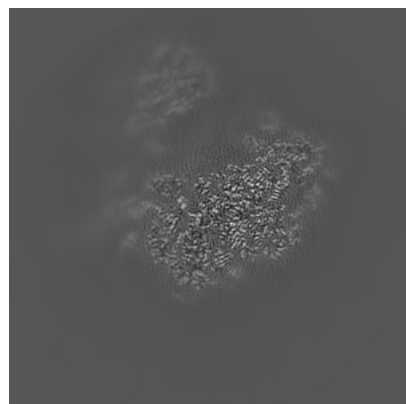


Z Index: 200

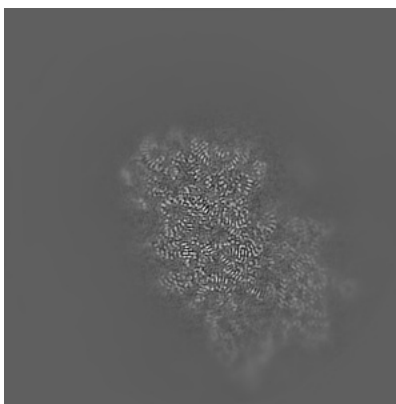
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

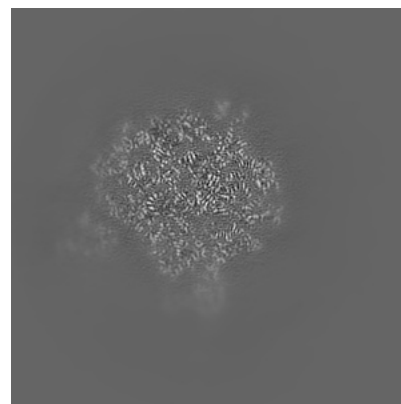
6.3.1 Primary map



X Index: 206



Y Index: 225

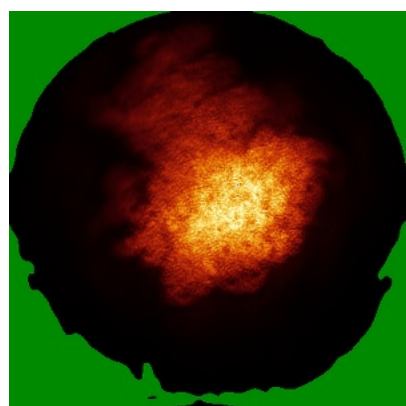


Z Index: 200

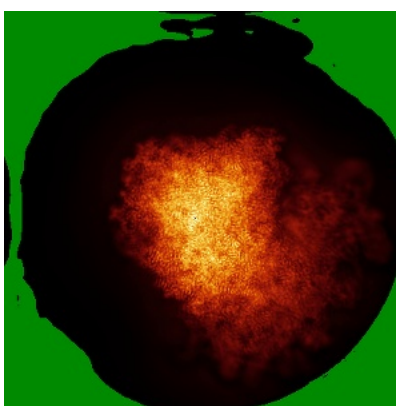
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

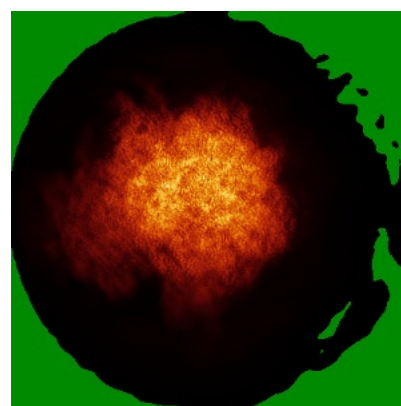
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

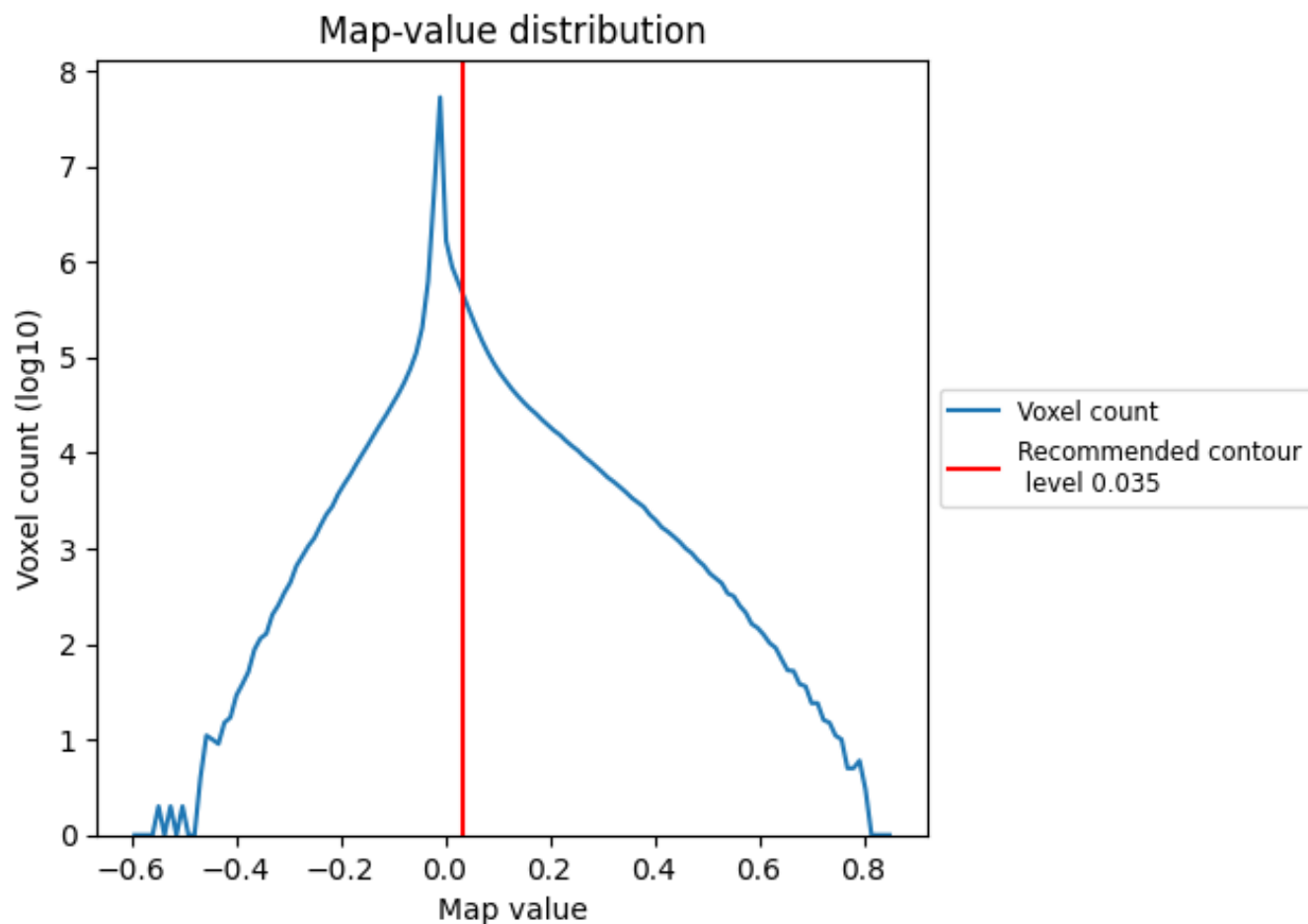
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

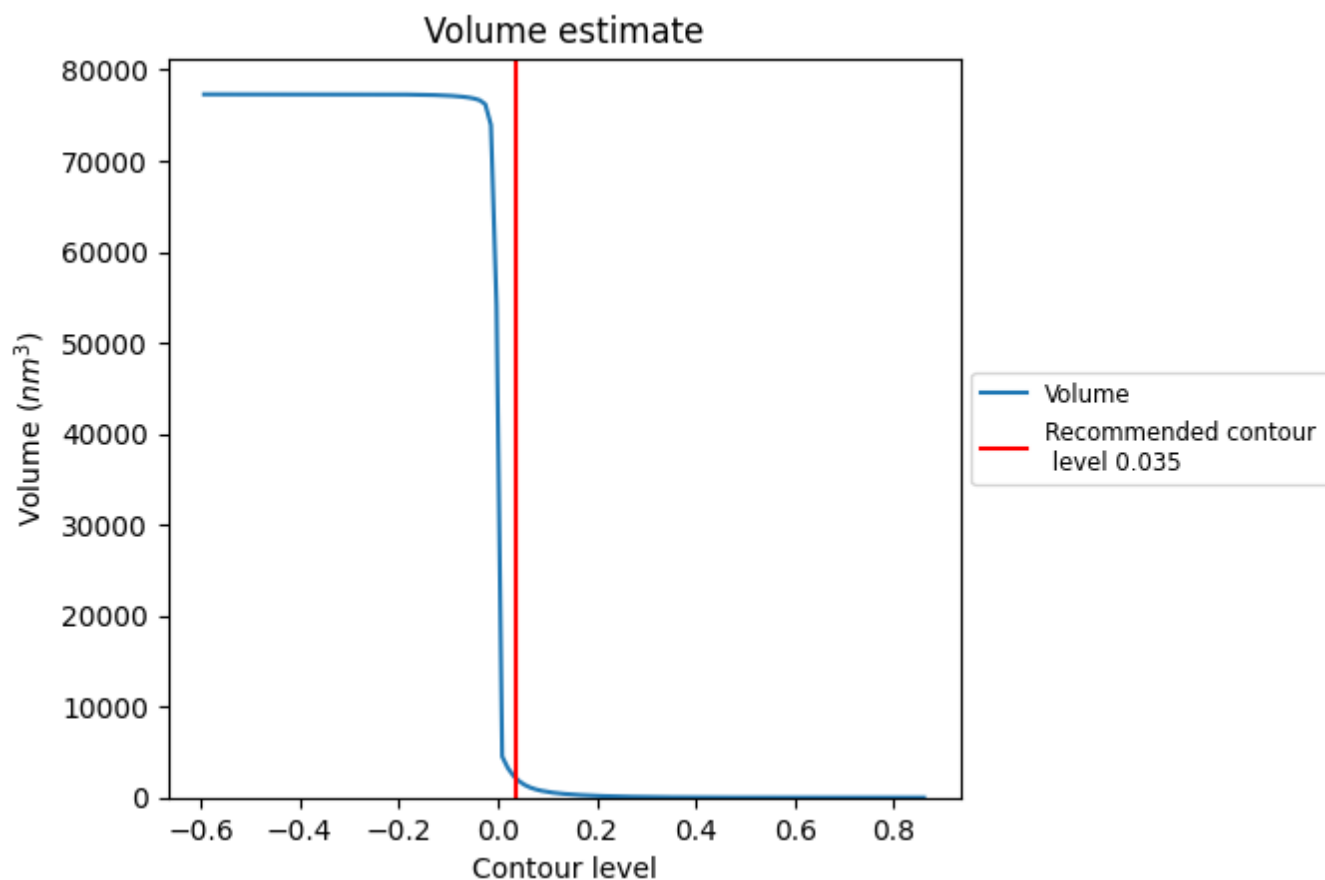
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

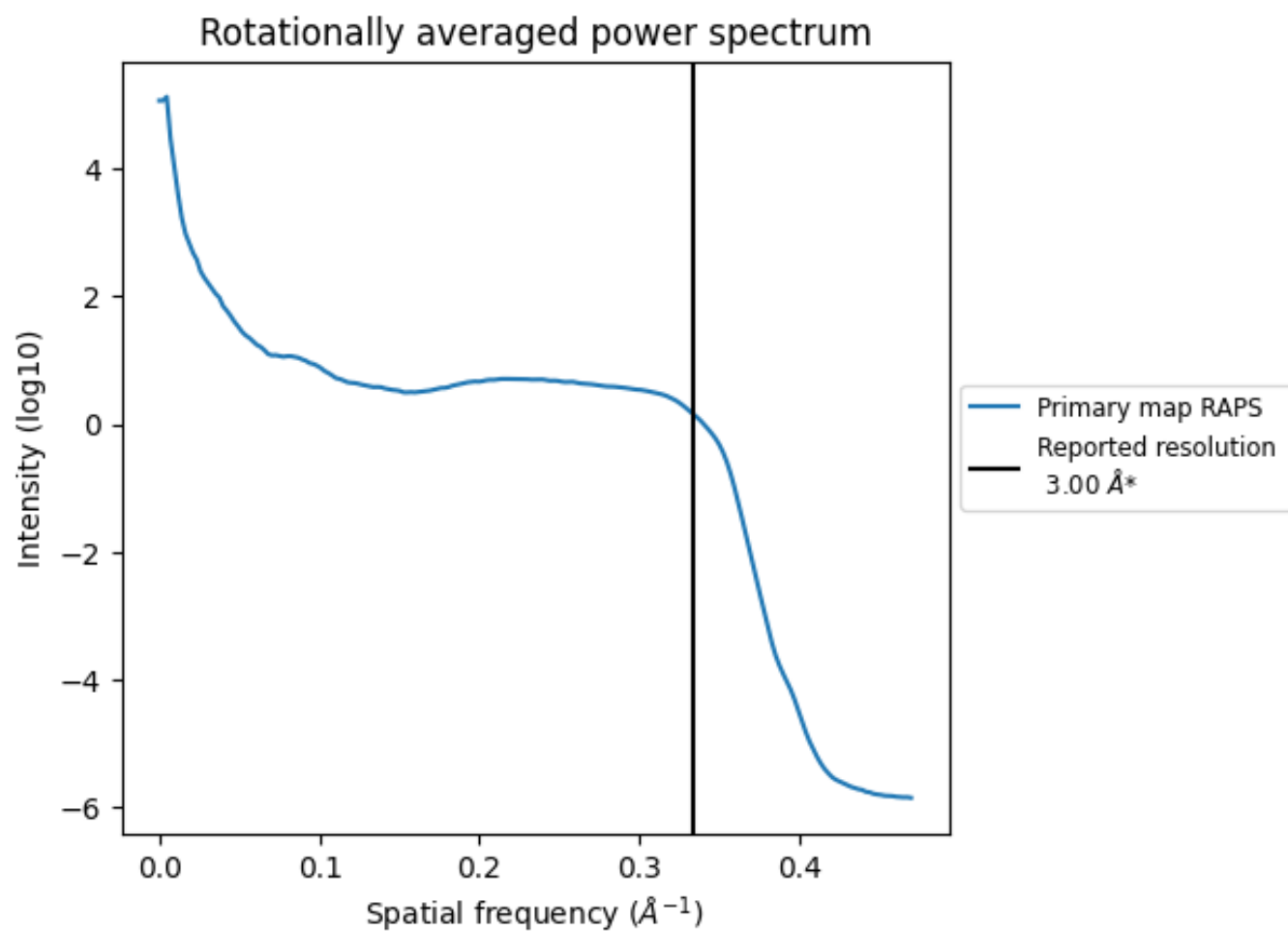
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2221 nm³; this corresponds to an approximate mass of 2007 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

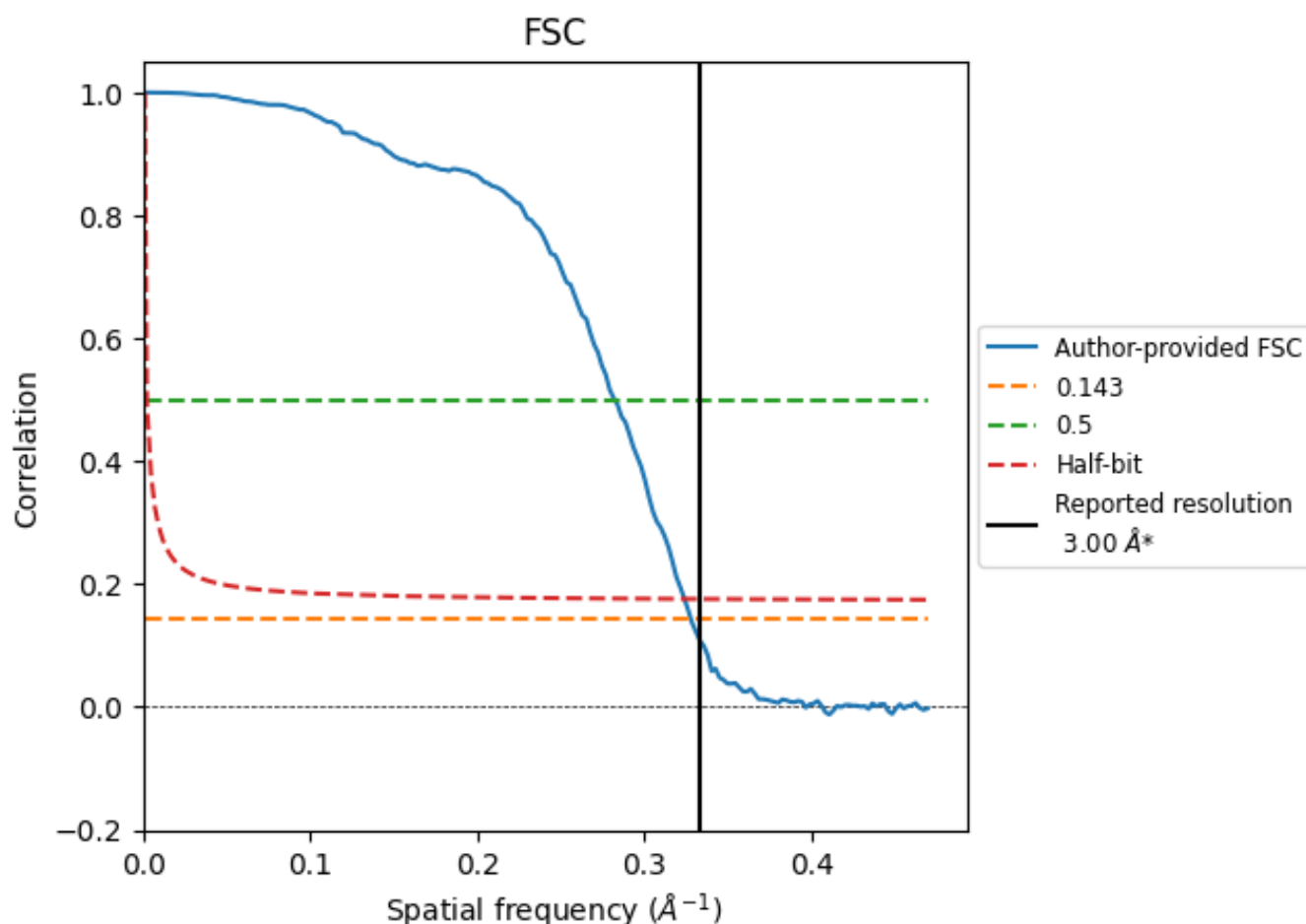


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

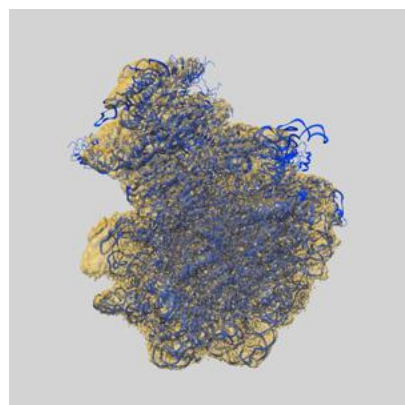
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.05	3.54	3.09
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

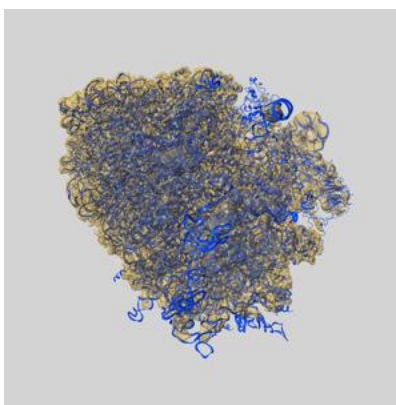
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10624 and PDB model 6XU8. Per-residue inclusion information can be found in section 3 on page 20.

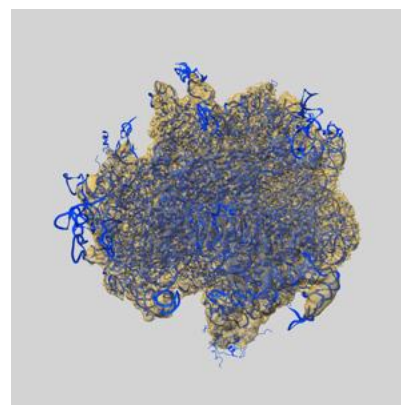
9.1 Map-model overlay [i](#)



X



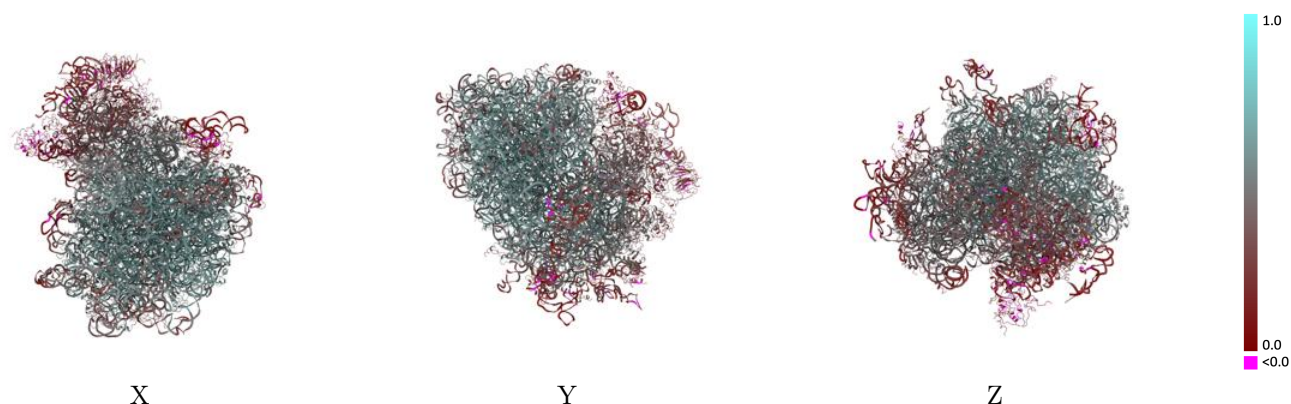
Y



Z

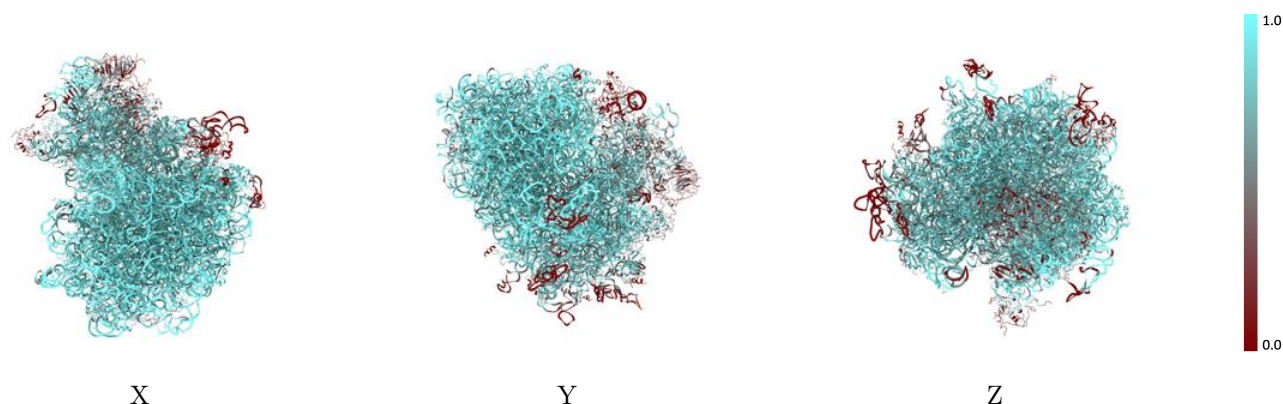
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



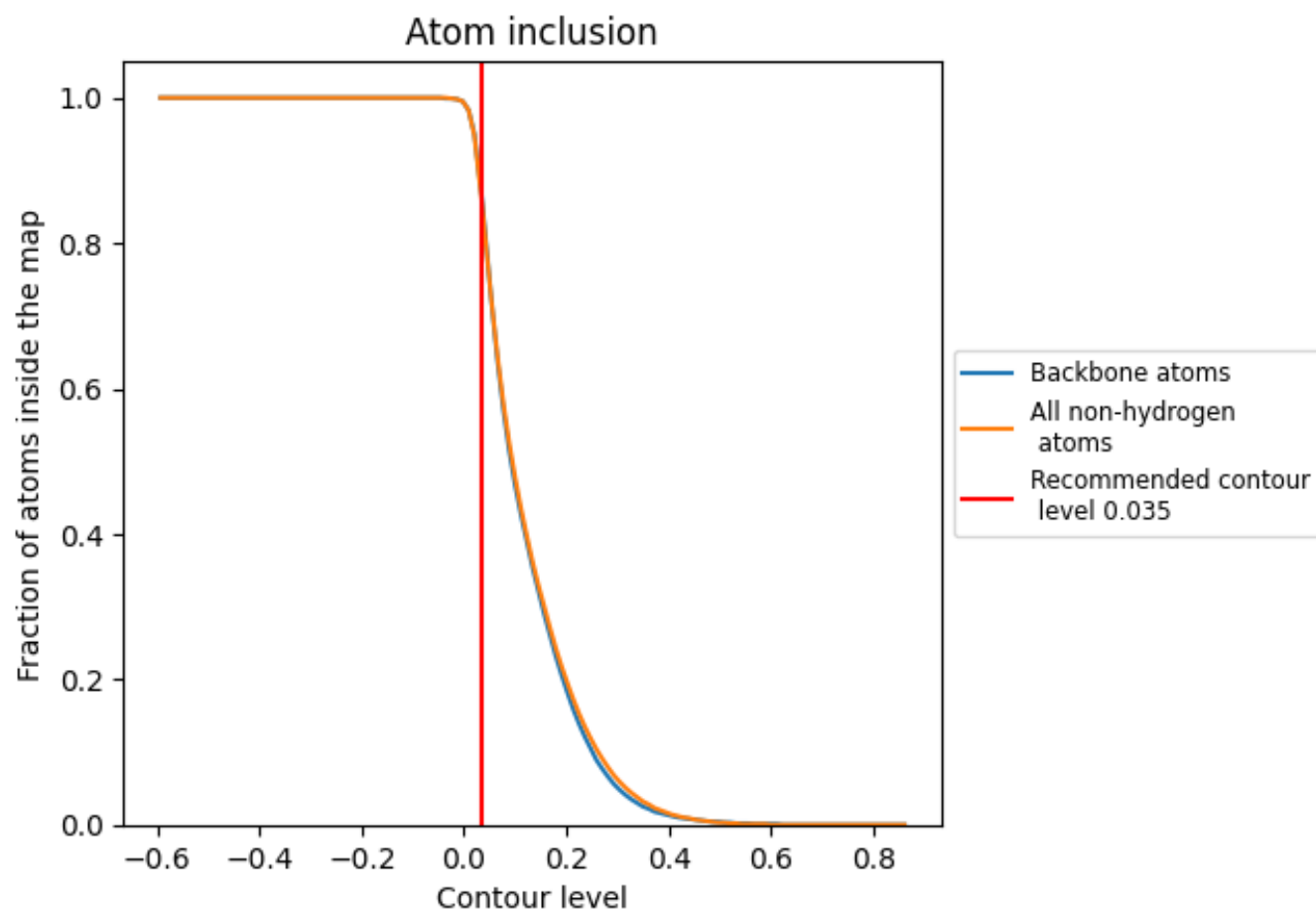
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.035).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8560	 0.4690
A5	 0.9300	 0.5240
A7	 0.9890	 0.5620
A8	 0.9790	 0.5900
A9	 0.9890	 0.5630
AA	 0.6440	 0.3570
AB	 0.7850	 0.4240
AC	 0.7080	 0.4180
AD	 0.4960	 0.2880
AE	 0.7810	 0.4400
AF	 0.4030	 0.2890
AG	 0.6770	 0.3620
AH	 0.6720	 0.3350
AI	 0.7140	 0.4450
AJ	 0.7860	 0.3840
AK	 0.8310	 0.1820
AL	 0.7310	 0.4760
AM	 0.3340	 0.0880
AN	 0.8370	 0.4940
AO	 0.8010	 0.4400
AP	 0.6410	 0.2030
AQ	 0.4760	 0.2430
AR	 0.3860	 0.2720
AS	 0.6640	 0.2790
AT	 0.6780	 0.2540
AU	 0.4620	 0.2850
AV	 0.6100	 0.3970
AW	 0.8340	 0.4890
AX	 0.7800	 0.4840
AY	 0.7450	 0.3580
AZ	 0.3970	 0.2280
Aa	 0.7760	 0.4720
Ab	 0.7900	 0.3890
Ac	 0.5360	 0.3050
Ad	 0.8290	 0.3120



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Chain	Atom inclusion	Q-score
Ae	 0.6000	 0.3500
Af	 0.4230	 0.0970
Ag	 0.2740	 0.1760
B2	 0.8560	 0.3880
CA	 0.9590	 0.5900
CB	 0.9340	 0.5680
CC	 0.9430	 0.5700
CD	 0.8930	 0.4970
CE	 0.8360	 0.4500
CF	 0.9770	 0.5970
CG	 0.8210	 0.4880
CH	 0.9590	 0.5270
CI	 0.8560	 0.4890
CJ	 0.8410	 0.4420
CL	 0.8710	 0.5180
CM	 0.9020	 0.4850
CN	 0.9670	 0.5880
CO	 0.9580	 0.5830
CP	 0.8400	 0.5490
CQ	 0.9720	 0.5970
CR	 0.8270	 0.4900
CS	 0.9540	 0.5590
CT	 0.9520	 0.5600
CU	 0.8200	 0.4670
CV	 0.9580	 0.5910
CW	 0.9510	 0.5770
CX	 0.9120	 0.5480
CY	 0.9670	 0.5800
CZ	 0.9260	 0.5180
Ca	 0.9520	 0.5710
Cb	 0.9330	 0.5120
Cc	 0.9350	 0.5380
Cd	 0.9530	 0.5620
Ce	 0.9680	 0.6060
Cf	 0.9070	 0.5050
Cg	 0.9730	 0.5870
Ch	 0.9340	 0.5600
Ci	 0.8650	 0.4810
Cj	 0.9780	 0.6210
Ck	 0.8650	 0.4890
Cl	 0.9810	 0.6090
Cm	 0.9740	 0.5340

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Chain	Atom inclusion	Q-score
Cn	 0.9350	 0.5760
Co	 0.9480	 0.5650
Cp	 0.9560	 0.5900
Cr	 0.8540	 0.5020
Cz	 0.0230	 0.1440